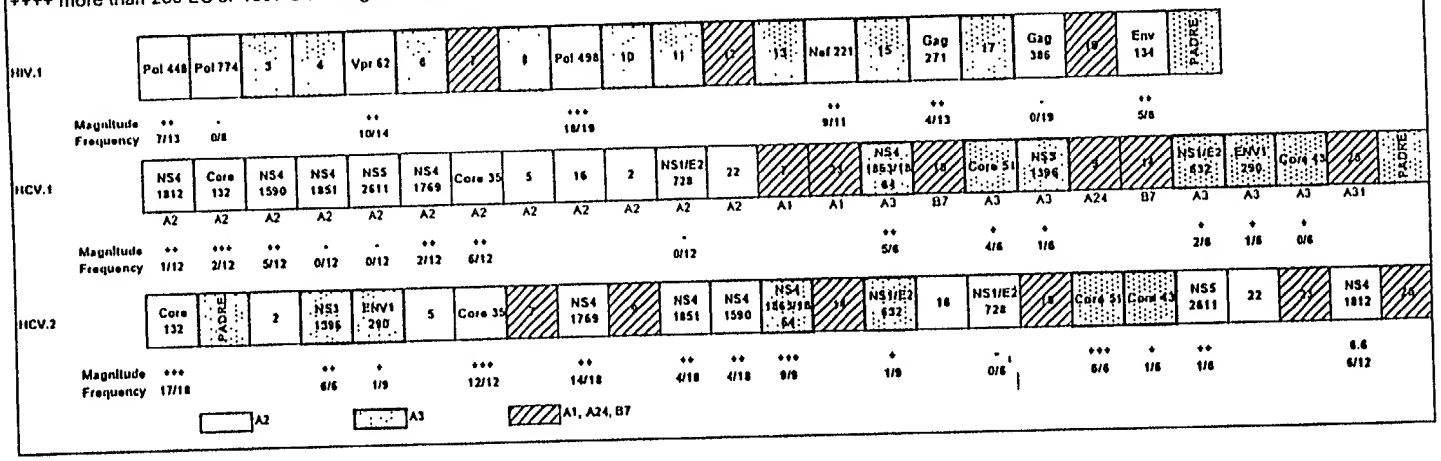
FIGURE 1

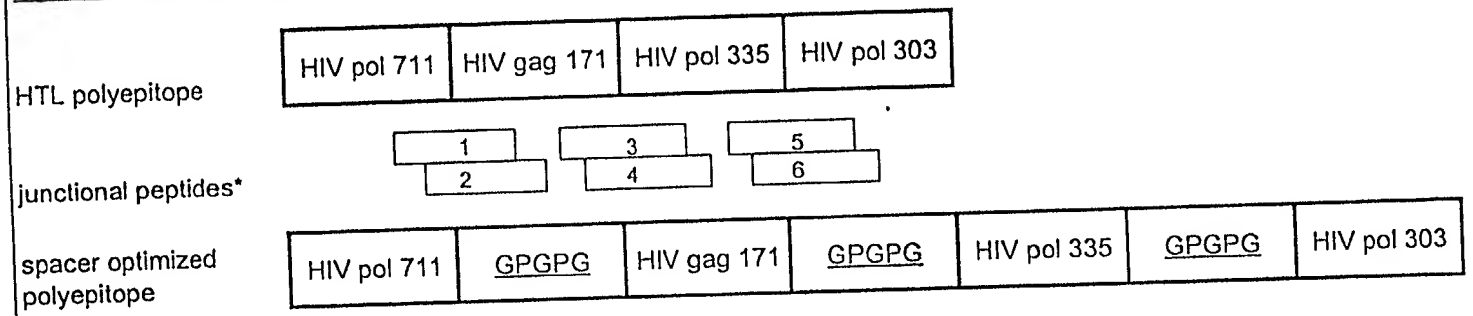
Figure 1. Immunogenicity of HIV- and HCV-derived minigenes in HLA transgenic animals.

Magnitude of CTL responses are stored as follows + up to 2 LU (Lytic Units) or 10 SV (Secretory Units); ++ up to 200 LU or 100 SU; +++ up to 200 LU or 1000 SU; ++++ more than 200 LU or 1000 SU. Magnitude represents number of independent cultures yielding positive responses.



TO/290 8F0h6860

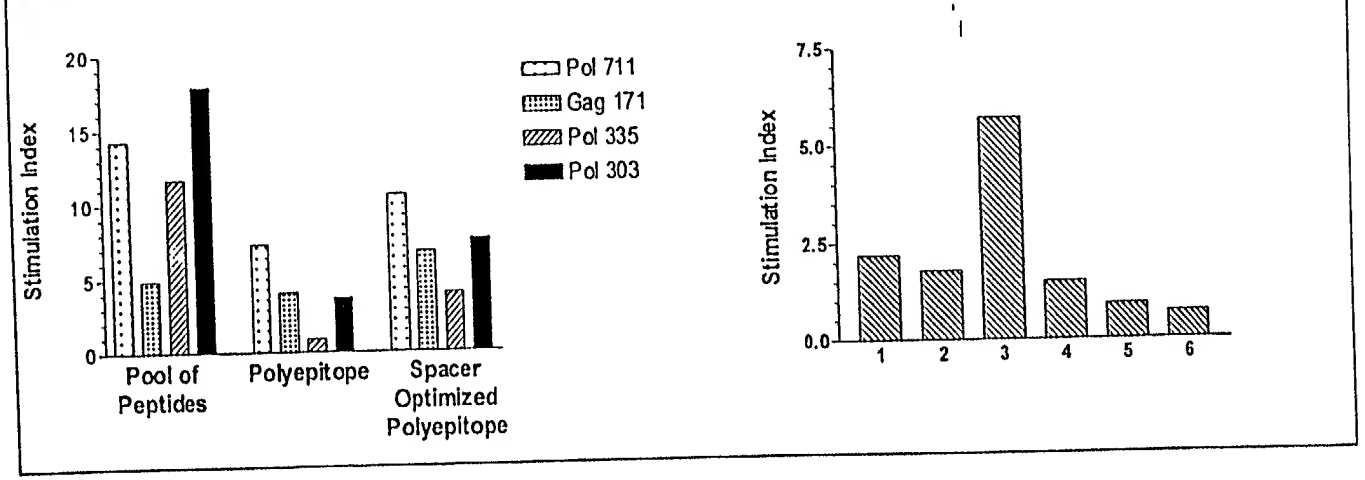
Figure 2a. Synthetic polypeptides encoding HIV-derived HTL epitopes



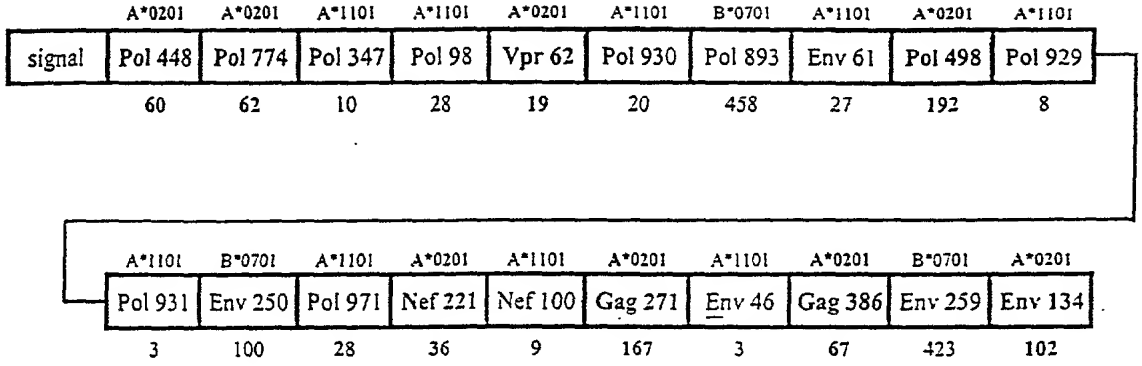
* junctional peptides comprise either 10 amino acids from the N-terminal epitope and 5 amino acids from the C-terminal epitope or 5 amino acids from the N-terminal epitope and 10 amino acids from the C-terminal epitope.

FIGURE 2

Figure 2b. Proliferative responses to synthetic polypeptides encoding HIV-derived HTL

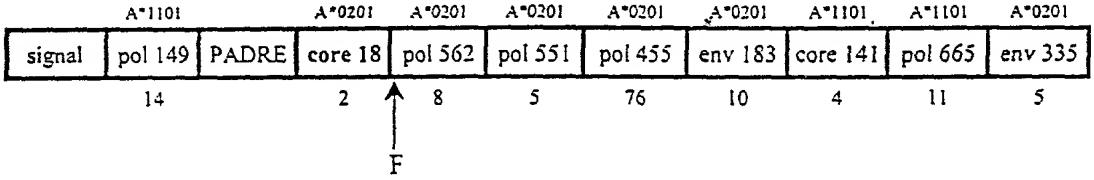


a : HIV-FT

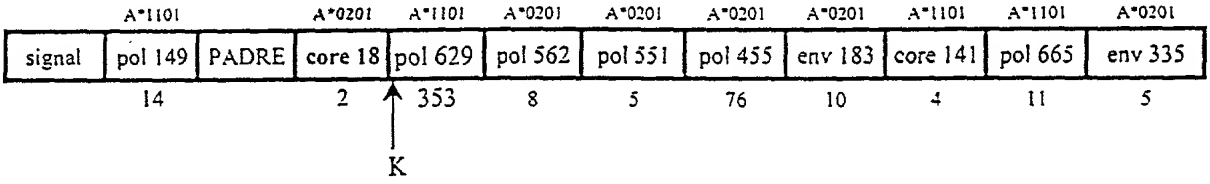


b : HBV-specific multiepitope constructs

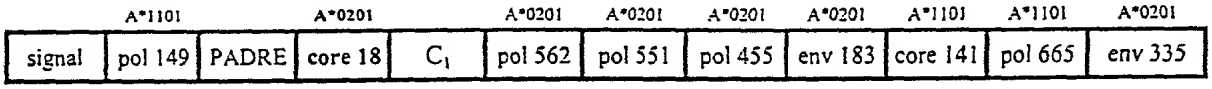
HBV.1



HBV.2

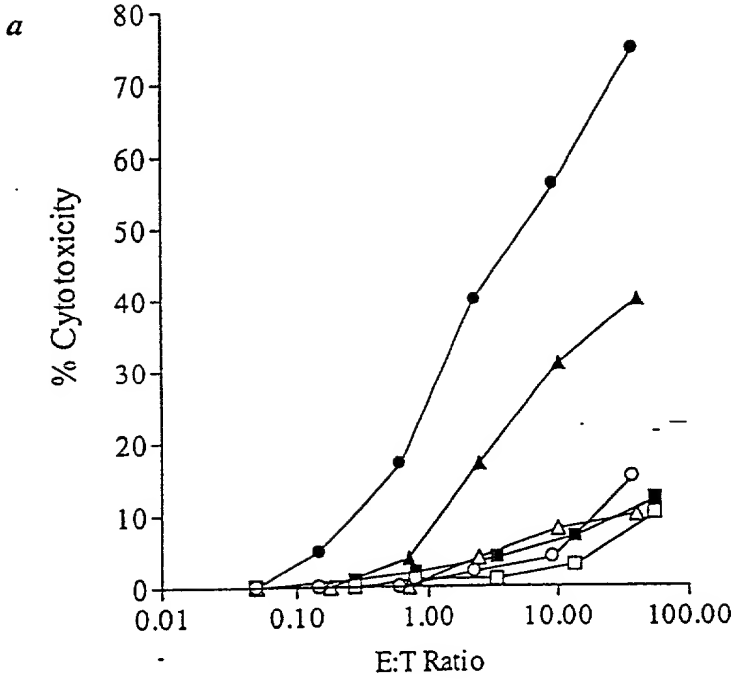


HBV.1X



C_1= either W, Y, L, K, R, C, N or G

FIGURE 3


a
% Cytotoxicity
80
70
60
50
40
30
20
10
0
0.01
0.10
1.00
10.00
100.00
E:T Ratio

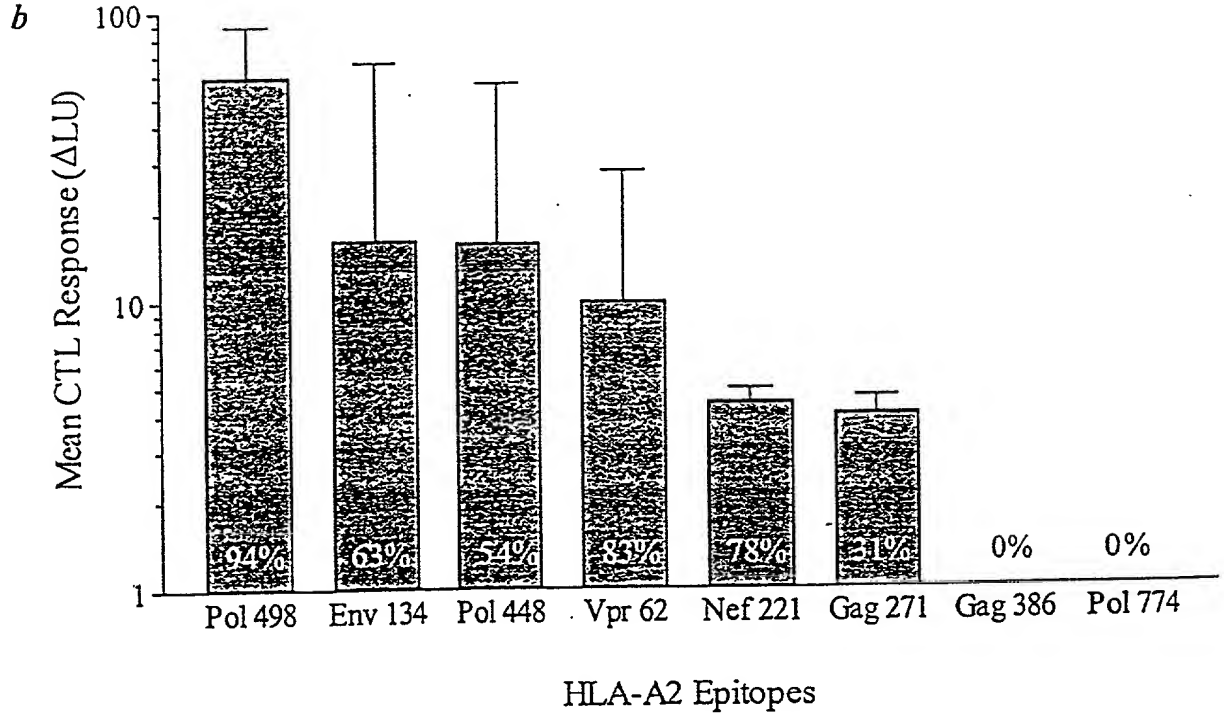

b
Mean CTL Response (ΔLU)
100
10
1
94%
63%
54%
83%
78%
31%
0%
0%
Pol 498
Env 134
Pol 448
Vpr 62
Nef 221
Gag 271
Gag 386
Pol 774
HLA-A2 Epitopes

FIGURE 4

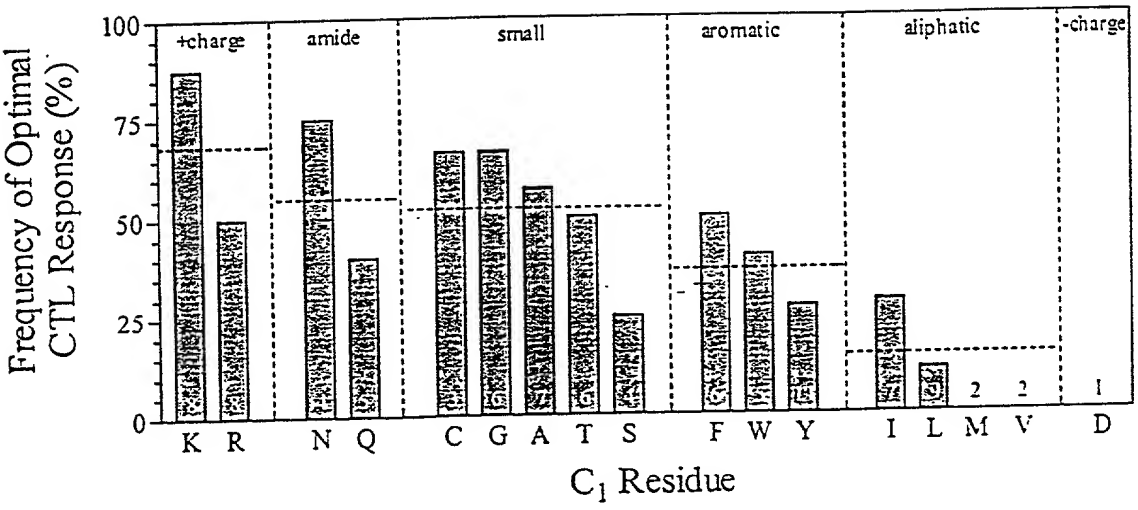
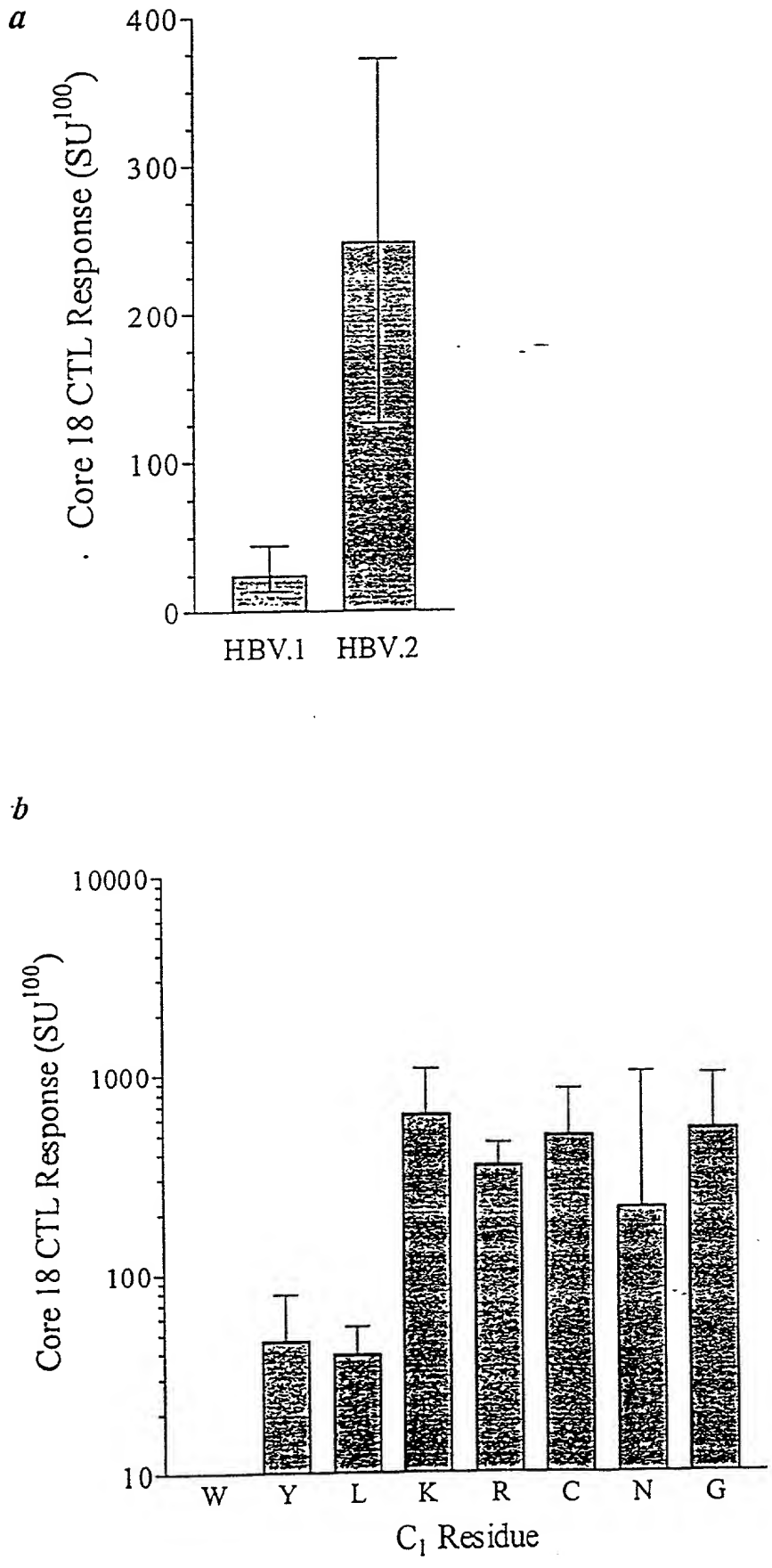

Frequency of Optimal CTL Response (%)
100
75
50
25
0
+charge
amide
small
aromatic
aliphatic
-charge
K R N Q C G A T S F W Y I L M V D
2 2 1
C1 Residue

FIGURE 5

FIGURE 6


a
400
300
200
100
0
Core 18 CTL Response (SU100)
HBV.1
HBV.2
b
10000
1000
100
10
Core 18 CTL Response (SU100)
W
Y
L
K
R
C
N
G
C1 Residue

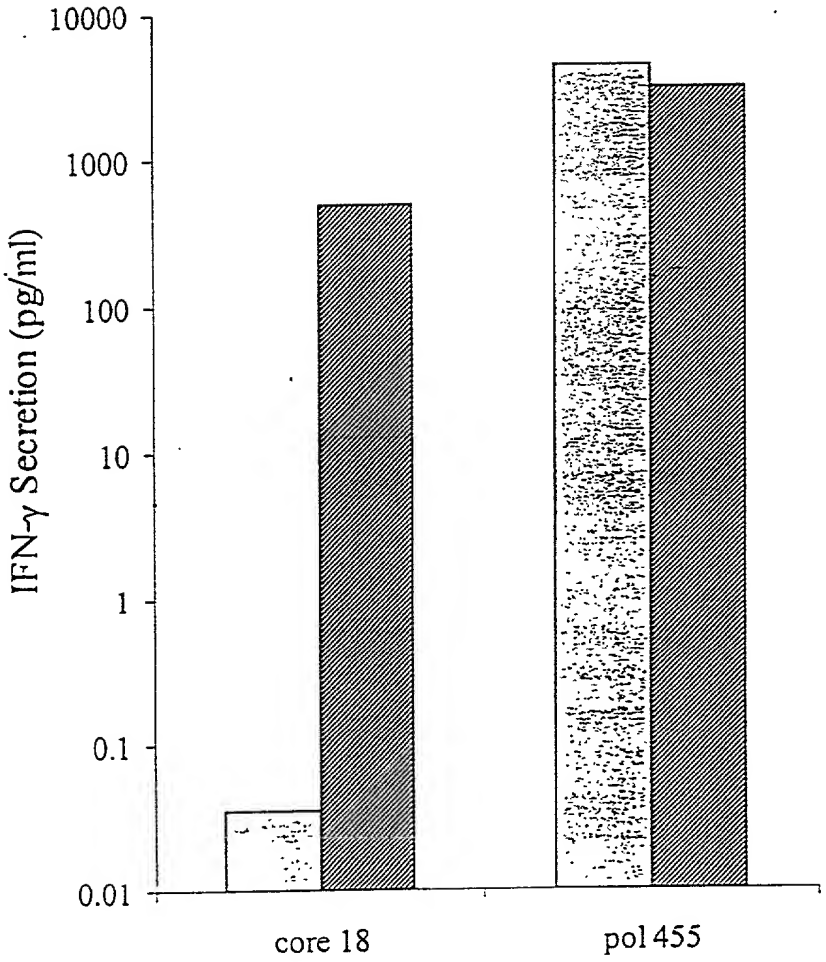


FIGURE 7

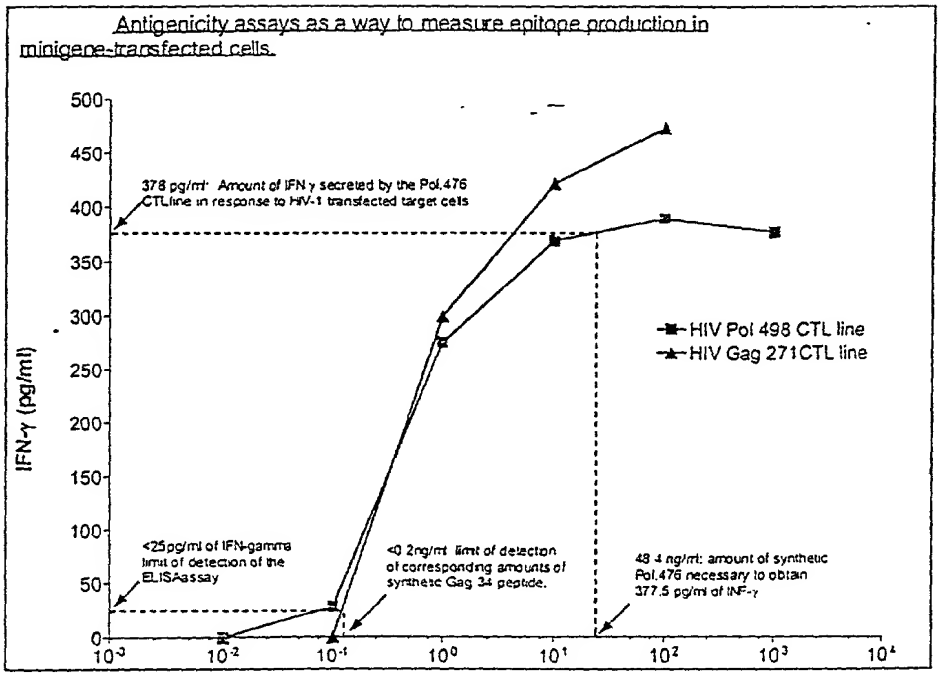
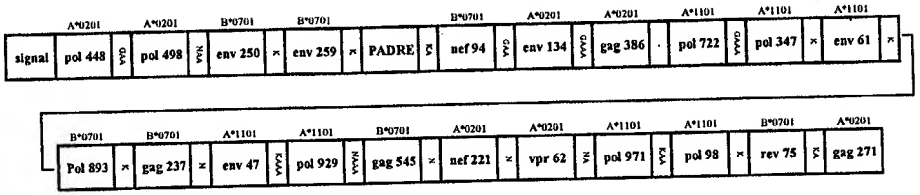

Antigenicity assays as a way to measure epitope production in minigene-transfected cells.
IFN-γ (pg/ml)
500
450
400
350
300
250
200
150
100
50
0
378 pg/ml: Amount of IFN γ secreted by the Pol.476 CTLline in response to HIV-1 transfected target cells
HIV Pol 498 CTL line
HIV Gag 271CTL line
<25pg/ml of IFN-gamma limit of detection of the ELISAassay
<0.2ng/ml limit of detecton of corresponding amounts of synthetic Gag 34 peptide.
48.4 ng/ml: amount of synthetic Pol.476 necessary to obtain 377.5 pg/ml of INF-γ
10-3
10-2
10-1
100
101
102
103
104

FIGURE 8

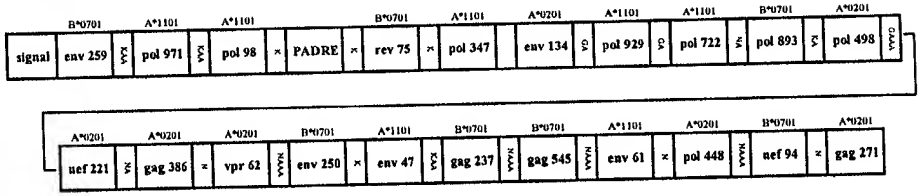
TC290 Attached

FIGURE 9

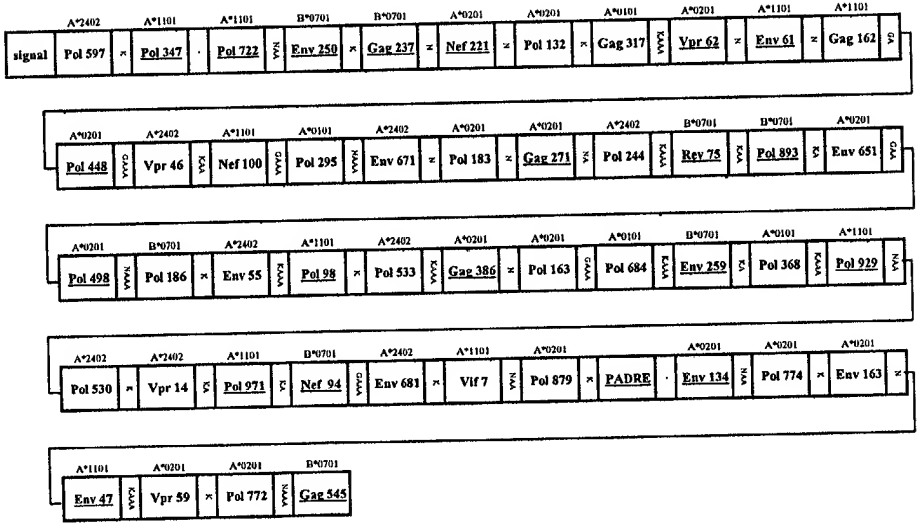
EP-HIV-1090



HIV-CPT



HIV-TC



TO/290 8FOn6860

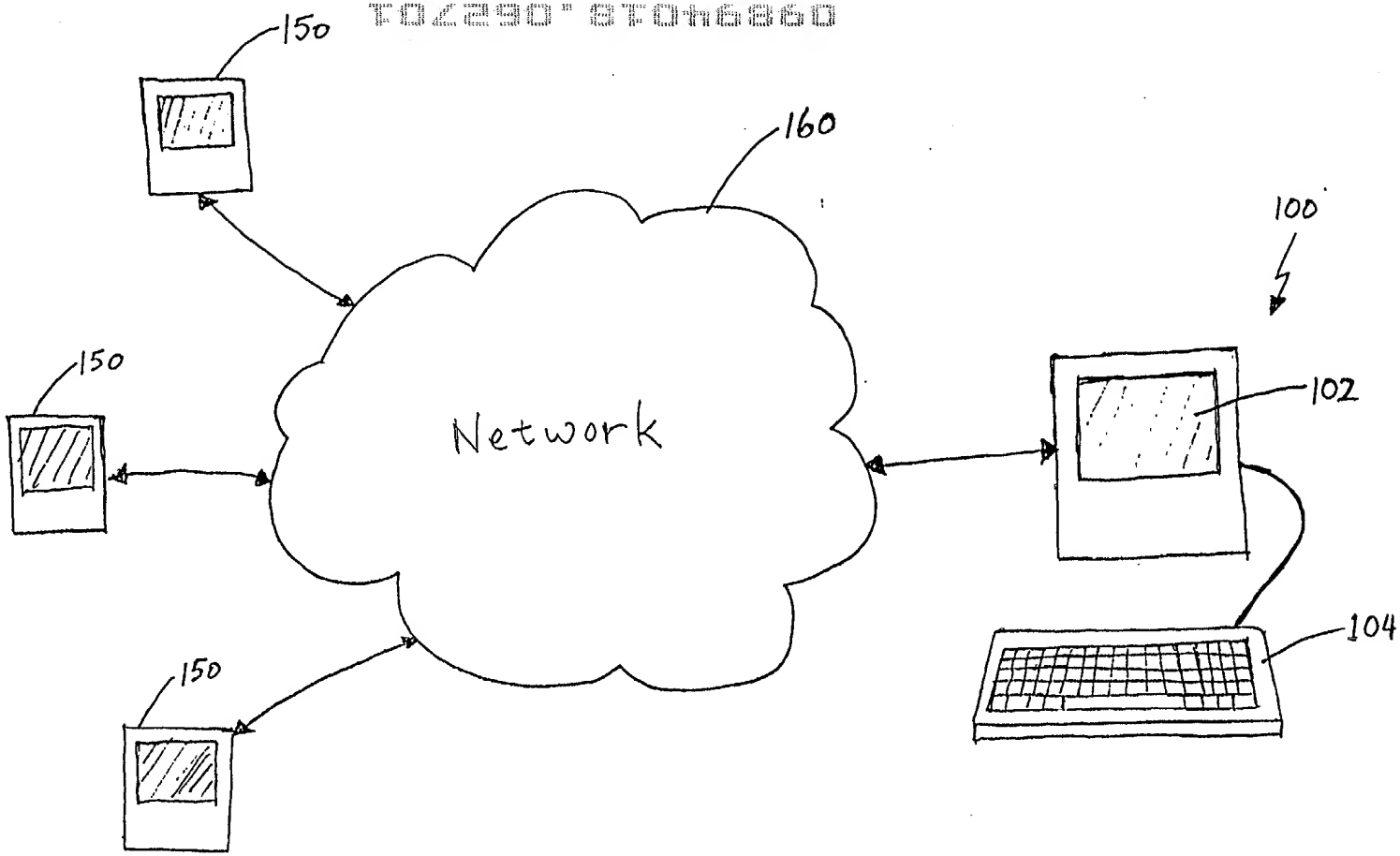


FIGURE 10

200

Sequence	Length	Code
VLAEAMSQV	9	A
ILKEPVHGV	9	B
TLNFPISPI	9	C
SLLNATDIAV	10	D
QMAVFIHNFK	10	E
VTVYYGVPVWK	11	F
FPVRPQVPL	9	G
YPLASLRSLF	10	H
VIYQYMDDLY	10	I
IYQEPFKNL	9	J
IWGCSGKLI	9	K

202

AA	C+1 ranking	N-1 ranking
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

204

Motif Specification

XXXX(FY)XX(LIMV)
XXXX(FY)XXX(LIMV)
XXXXNXXX(LIMV)
XXXXNXXXX(LIMV)
X(LM)XXXXXXV
X(LM)XXXXXXXV
X(LMVT)XXXXXX(KRY)
X(LMVT)XXXXXXX(KRY)
XPXXXXXX(LIMVF)
XPXXXXXXX(LIMVF)

206

FIGURE 11A

MaxInsertions={enter value here} 208

OutputToScreen=yes/no 210

OutputToFile=yes/no 212

MinimumAccepted={enter value here} 214

MaxDuplicateFunctionValues={enter value here} 216

MaxSearchTime (min.)={enter value here} 218

Exhaustive=yes/no 220

NumStochasticProbes={enter value here} 222

MaxHitsPerProbe={enter value here} 224

RandomProbeStart=yes/no 226

FIGURE 11B

Docket No. 95-2-5

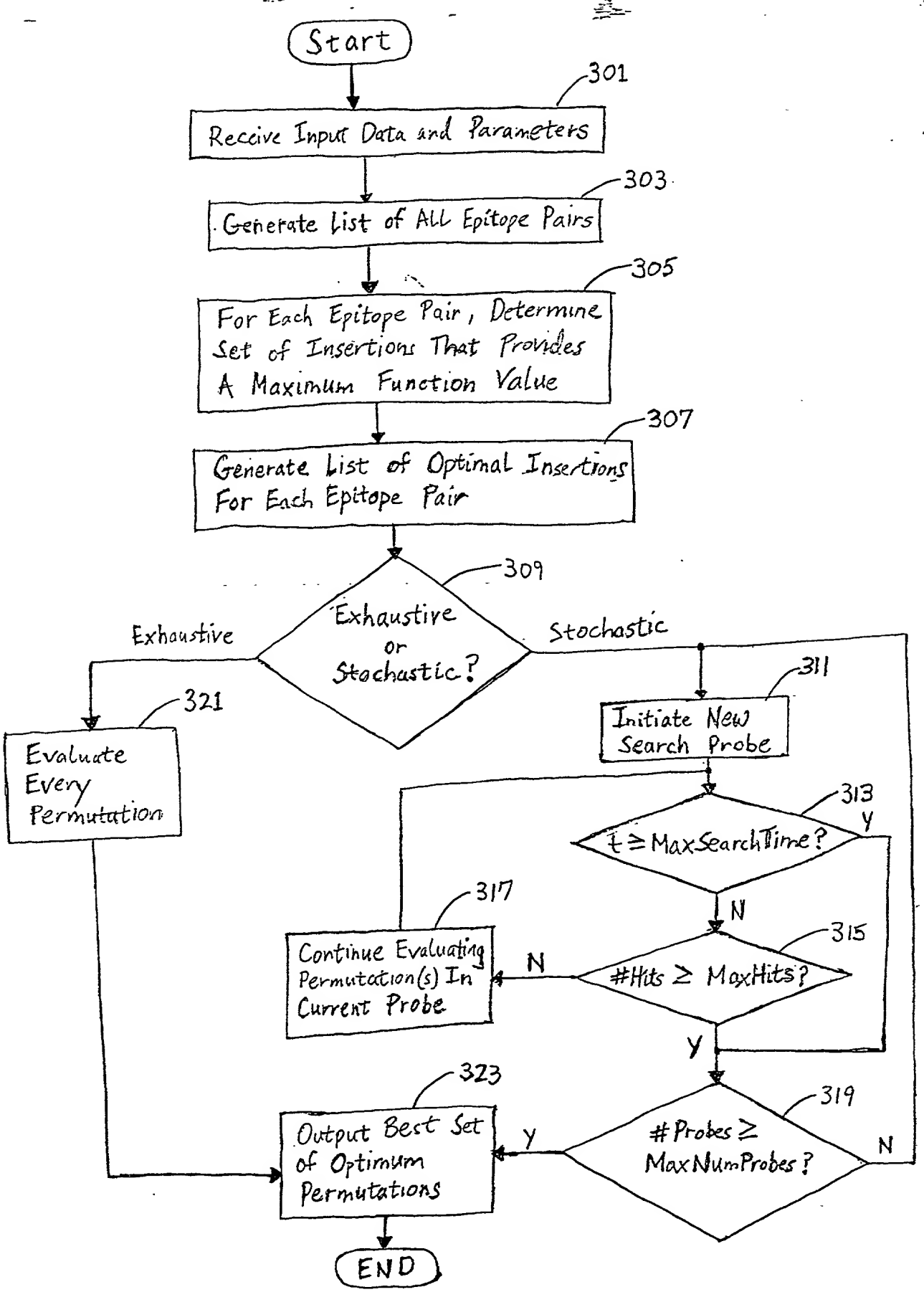

Start
301
Receive Input Data and Parameters
303
Generate List of ALL Epitope Pairs
305
For Each Epitope Pair, Determine Set of Insertions That Provides A Maximum Function Value
307
Generate List of Optimal Insertions For Each Epitope Pair
309
Exhaustive or Stochastic?
Exhaustive
Stochastic
321
Evaluate Every Permutation
311
Initiate New Search Probe
313
t ≥ MaxSearchTime?
Y
N
315
#Hits ≥ MaxHits?
N
317
Continue Evaluating Permutation(s) In Current Probe
Y
319
Probes ≥ MaxNumProbes?
Y
N
323
Output Best Set of Optimum Permutations
END

FIGURE 12

Junctional Analyzer run on Saturday, February 26, 2000 09:06:23 pm.

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.33
G	1.33	1.80
I	0.50	0.86
K	0.64	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

204

The following 10 motif specifications will be used to search for junctionals.

Count	Motif Specification
1	XXXX(FY)XX(LIMV)
2	XXXX(FY)XXX(LIMV)
3	XXXXNXXX(LIMV)
4	XXXXNXXXX(LIMV)
5	X(LM)XXXXXXV
6	X(LM)XXXXXXXV
7	X(LMVT)XXXXXX(KRY)
8	X(LMVT)XXXXXXX(KRY)
9	XPXXXXXX(LIMVF)
10	XPXXXXXXX(LIMVF)

206

Code	Peptide	Length
A	VLAEAMSQV	9
B	ILKEPVHGV	9
C	TLNFPISPI	9
D	SLLNATDIAV	10
E	QMAVFIHNFK	10
F	VTVYYGVPVWK	11
G	FPVRPQVPL	9
H	YPLASLRSLF	10
I	VIYQYMDDLY	10
J	IYQEPFKNL	9
K	IWGCSGKLI	9

202

MaxInsertions = 4 (208)

FIGURE 13A

09594018 - 022699

OutputToScreen = No

OutputToFile = Yes

MinimumValueAccepted = 0

MaxDuplicateFunctionValues = 50

SearchTime = 5

NumStochasticProbes = 10

MaxHitsPerProbe = 25

RandomProbeStart = Yes

Col. 1 Code 1	Col. 2 I1	Col. 3 I2	Col. 4 I3	Col. 5 I4	Col. 6 Code 2	Col. 7 C	Col. 8 N	Col. 9 C+N	Col. 10 J	Col. 11 MaxFunc.
A	C	A		L	B	2.00	2.20	4.40	0	8.80
A	C			L	C	2.00	2.20	4.40	0	8.80
A	C			L	D	2.00	2.20	4.40	0	8.80
A	C			L	E	2.00	2.20	4.40	0	8.80
A	C			R	F	2.00	1.57	3.14	2	1.57
A	C			R	G	2.00	1.57	3.14	1	3.14
A	C			R	H	2.00	1.57	3.14	0	6.28
A	G				I	1.80	1.33	2.39	1	2.39
A	C	A	A	G	J	2.00	1.33	2.66	0	5.32
A	C			R	K	2.00	1.57	3.14	0	6.28
B	C	A	A	G	A	2.00	1.33	2.66	0	5.32
B	C	A		R	C	2.00	1.57	3.14	0	6.28
B	C	A		R	D	2.00	1.57	3.14	0	6.28
B	C	A		R	E	2.00	1.57	3.14	0	6.28
B	C	A	A	G	F	2.00	1.33	2.66	1	2.66
B	C			R	G	2.00	1.57	3.14	1	3.14
B	C			R	H	2.00	1.57	3.14	0	6.28
B	C	A	A	G	I	2.00	1.33	2.66	1	2.66
B	C	A	A	G	J	2.00	1.33	2.66	0	5.32
B	C	A	A	G	K	2.00	1.33	2.66	0	5.32
C	C	A		R	A	2.00	1.57	3.14	1	3.14
C	C	A		R	B	2.00	1.57	3.14	1	3.14
C	C			L	D	2.00	2.20	4.40	1	4.40
C	C	A		R	E	2.00	1.57	3.14	1	3.14
C	C			R	F	2.00	1.57	3.14	1	3.14
C	C			R	G	2.00	1.57	3.14	1	3.14
C	C			R	H	2.00	1.57	3.14	0	6.28
C	C	A		R	I	2.00	1.57	3.14	1	3.14
C	C	A	A	R	J	2.00	1.57	3.14	0	6.28
C	C	A	A	R	K	2.00	1.57	3.14	0	6.28

FIGURE 13B

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
D	C			L	A	2.00	2.20	4.40	0	8.80
D	C			L	B	2.00	2.20	4.40	0	8.80
D	C			L	C	2.00	2.20	4.40	0	8.80
D	C			L	E	2.00	2.20	4.40	0	8.80
D	G				F	1.80	1.33	2.39	0	4.79
D	C			R	G	2.00	1.57	3.14	0	6.28
D	C	A	A	G	H	2.00	1.33	2.66	0	5.32
D	C			L	I	2.00	2.20	4.40	1	4.40
D	C	A		G	J	2.00	1.33	2.66	0	5.32
D	C			R	K	2.00	1.57	3.14	0	6.28
E	C	A	A	L	A	2.00	2.20	4.40	0	8.80
E	C	A	A	L	B	2.00	2.20	4.40	0	8.80
E	C	A	A	L	C	2.00	2.20	4.40	0	8.80
E	C	A	A	L	D	2.00	2.20	4.40	0	8.80
E	C	A		R	F	2.00	1.57	3.14	0	6.28
E	C	A		R	G	2.00	1.57	3.14	0	6.28
E	C	A		R	H	2.00	1.57	3.14	0	6.28
E	C	A	A	L	I	2.00	2.20	4.40	0	8.80
E	C	A		R	J	2.00	1.57	3.14	0	6.28
E	C	A		R	K	2.00	1.57	3.14	0	6.28
F	K			L	A	2.20	2.20	4.84	1	4.84
F	K	A	A	G	B	2.20	1.33	2.93	1	2.93
F	K	A	A	G	C	2.20	1.33	2.93	0	5.85
F	K	A	A	G	D	2.20	1.33	2.93	0	5.85
F	K	A	A	G	E	2.20	1.33	2.93	0	5.85
F	K	A		G	G	2.20	1.33	2.93	1	2.93
F	K	A		G	H	2.20	1.33	2.93	1	2.93
F	K	A	A	G	I	2.20	1.33	2.93	1	2.93
F	K			R	J	2.20	1.57	3.45	1	3.45
F	K			R	K	2.20	1.57	3.45	0	6.91
G	C	A		R	A	2.00	1.57	3.14	1	3.14
G	C	A		R	B	2.00	1.57	3.14	2	1.57
G	C	A		R	C	2.00	1.57	3.14	1	3.14
G	C			L	D	2.00	2.20	4.40	1	4.40
G	C	A		R	E	2.00	1.57	3.14	2	1.57
G	C			L	F	2.00	2.20	4.40	4	1.10
G	C			G	H	2.00	1.33	2.66	0	5.32
G	C	A	A	R	I	2.00	1.57	3.14	2	1.57
G	C	A	A	R	J	2.00	1.57	3.14	1	3.14
G	C	A	A	R	K	2.00	1.57	3.14	0	6.28
H	C	A	A	G	A	2.00	1.33	2.66	0	5.32
H	C	A	A	G	B	2.00	1.33	2.66	1	2.66
H	C	A		G	C	2.00	1.33	2.66	0	5.32
H	C	A		G	D	2.00	1.33	2.66	0	5.32
H	C	A	A	G	E	2.00	1.33	2.66	0	5.32
H	C	A	A	G	F	2.00	1.33	2.66	1	2.66
H	C			R	G	2.00	1.57	3.14	1	3.14
H	C	A	A	G	I	2.00	1.33	2.66	1	2.66
H	C	A		G	J	2.00	1.33	2.66	1	2.66
H	C	A	A	G	K	2.00	1.33	2.66	0	5.32

20050260-0004

FIGURE 13C

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
I	K	A	A	G	A	2.20	1.33	2.93	0	5.85
I	K	A	A	G	B	2.20	1.33	2.93	1	2.93
I	K	A		G	C	2.20	1.33	2.93	0	5.85
I	K	A		G	D	2.20	1.33	2.93	0	5.85
I	K	A	A	G	E	2.20	1.33	2.93	0	5.85
I	K	A	A	G	F	2.20	1.33	2.93	1	2.93
I	K			R	G	2.20	1.57	3.45	1	3.45
I	K	A	A	G	H	2.20	1.33	2.93	0	5.85
I	K	A		G	J	2.20	1.33	2.93	1	2.93
I	K	A	A	G	K	2.20	1.33	2.93	0	5.85
J	K	A	A	R	A	2.20	1.57	3.45	0	6.91
J	K	A	A	R	B	2.20	1.57	3.45	1	3.45
J	K	A		R	C	2.20	1.57	3.45	0	6.91
J	K	A		R	D	2.20	1.57	3.45	0	6.91
J	K	A		R	E	2.20	1.57	3.45	1	3.45
J	K	A	A	R	F	2.20	1.57	3.45	2	1.73
J	K			R	G	2.20	1.57	3.45	1	3.45
J	K			R	H	2.20	1.57	3.45	0	6.91
J	K	A	A	R	I	2.20	1.57	3.45	1	3.45
J	K	A	A	R	K	2.20	1.57	3.45	0	6.91
K	K			L	A	2.20	2.20	4.84	0	9.68
K	K			L	B	2.20	2.20	4.84	0	9.68
K	K			L	C	2.20	2.20	4.84	0	9.68
K	K			L	D	2.20	2.20	4.84	0	9.68
K	K	A	A	L	E	2.20	2.20	4.84	0	9.68
K	K	A	A	R	F	2.20	1.57	3.45	1	3.45
K	G				G	1.80	1.33	2.39	0	4.79
K	K			R	H	2.20	1.57	3.45	0	6.91
K	K			L	I	2.20	2.20	4.84	1	4.84
K	K			R	J	2.20	1.57	3.45	0	6.91

Junctional Analyzer took 142.77 seconds.

EVS0-8E1-4P8

FIGURE 13D

T02290 "STOn6860

Figure 3a: CTL responses induced by EP HIV-1090 relative to individual peptides in IFA

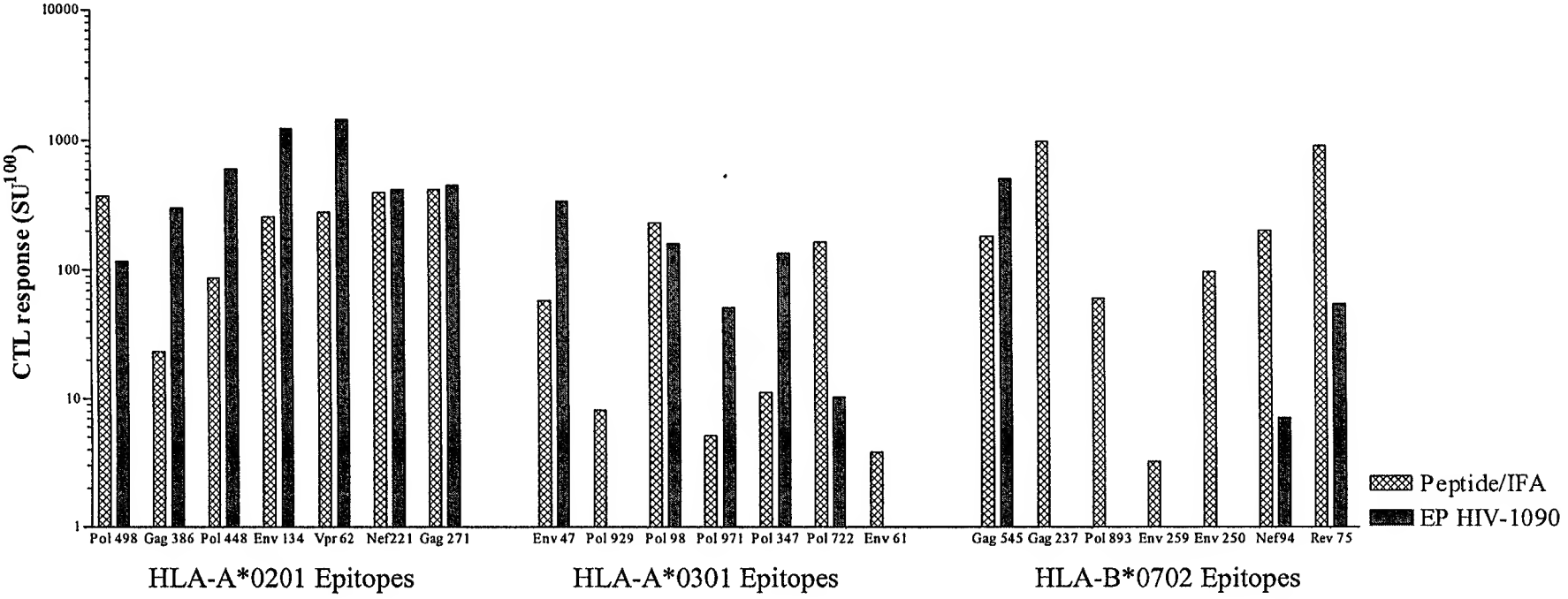
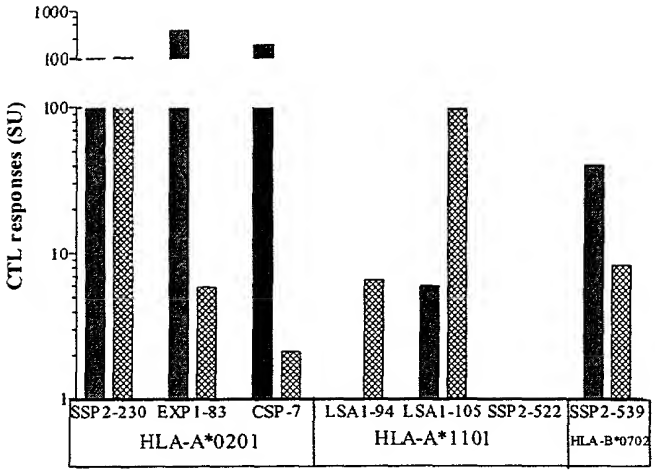


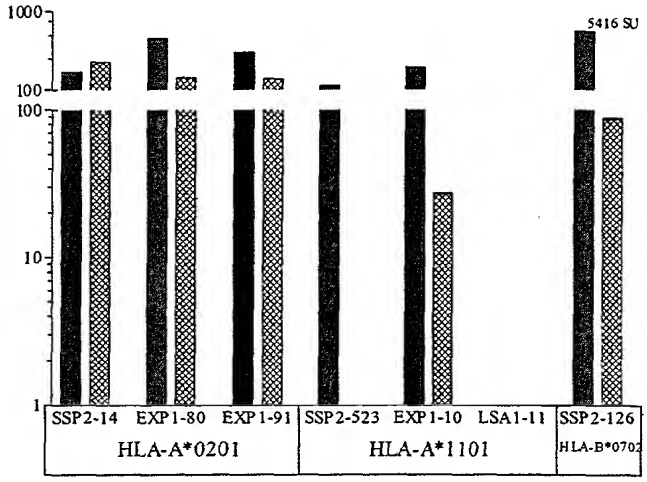
FIGURE 14A

Patent Application Publication Sep. 18, 2003 Sheet 14 of 15 US 2003/0175290 A1

Responses to PfCTL 1



Responses to PfCTL 2



Responses to PfCTL 3

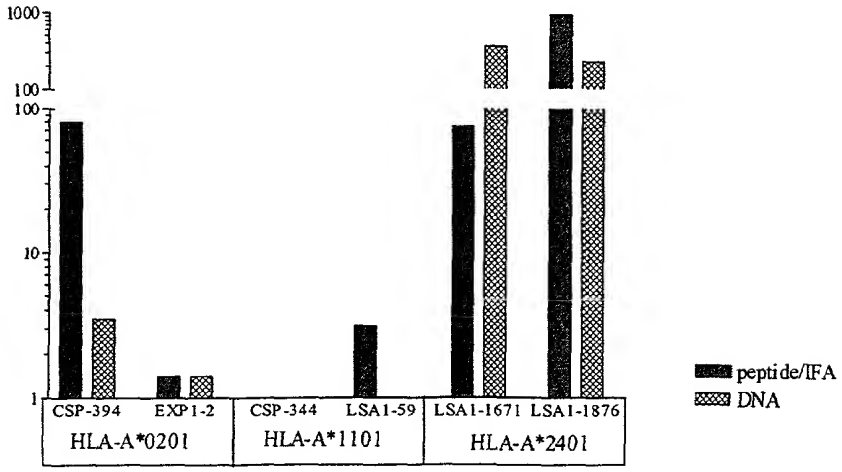


FIGURE 14B

TO2290 BTOR6860

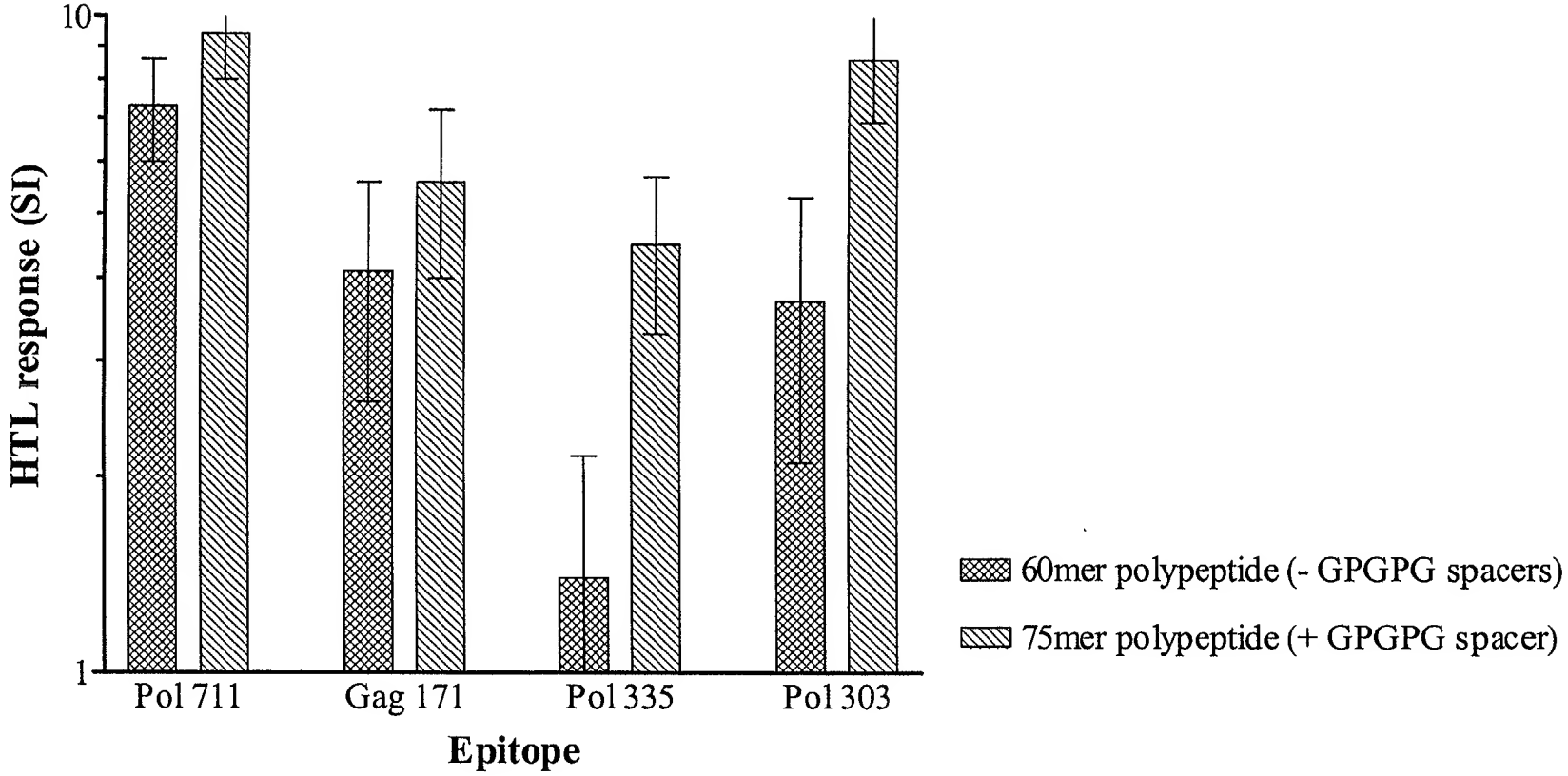


FIGURE 15

TO2290 "STD06860

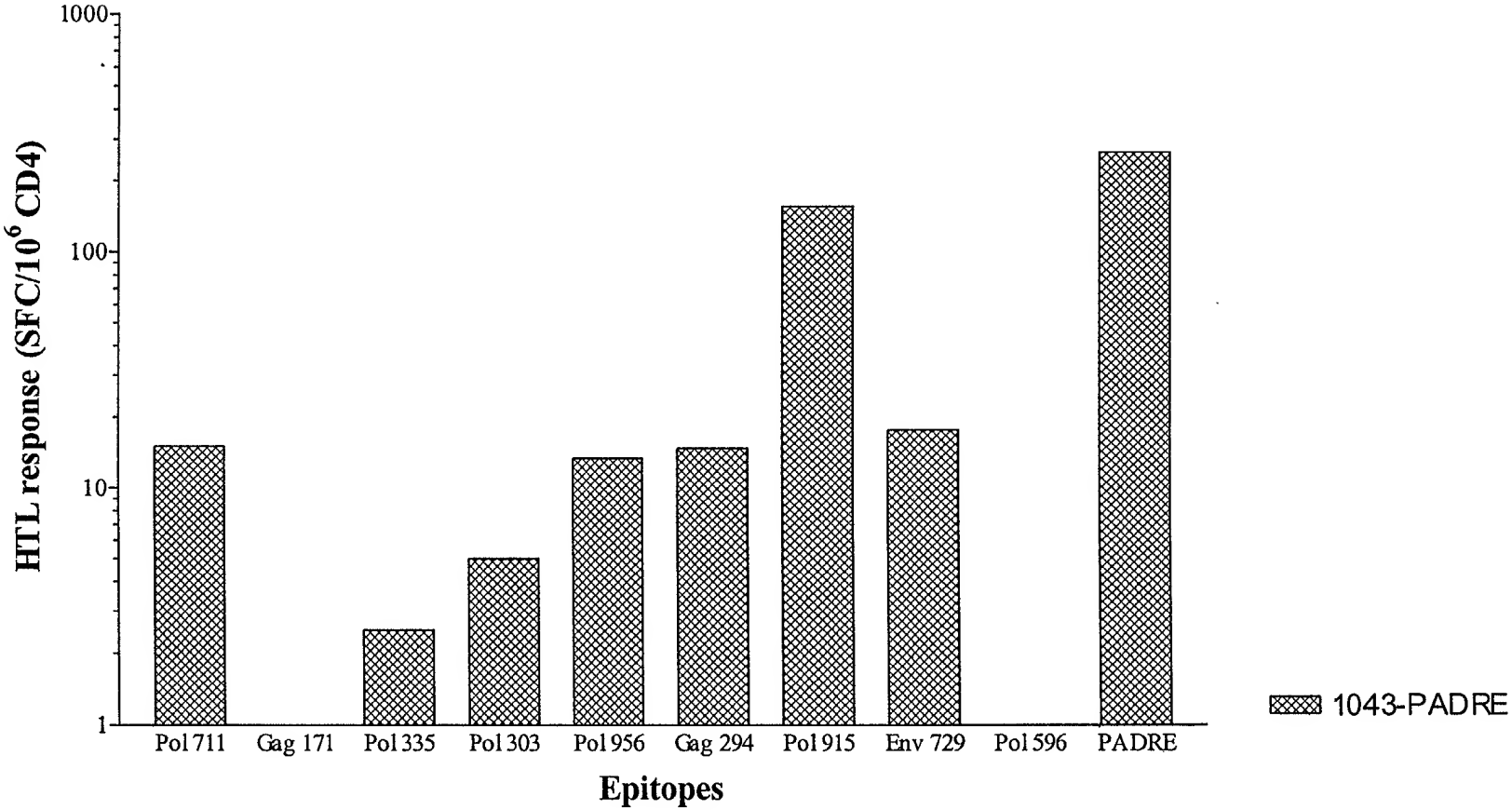
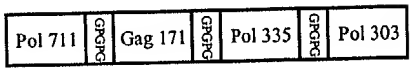


FIGURE 16

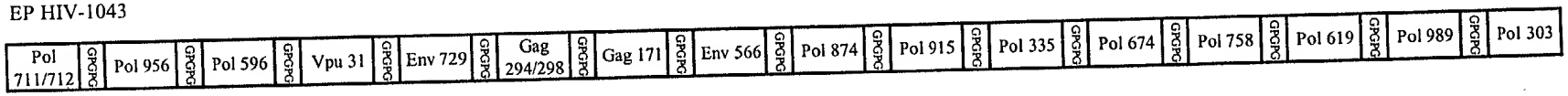
TO2290 B1 08/06/2860

FIGURE 17

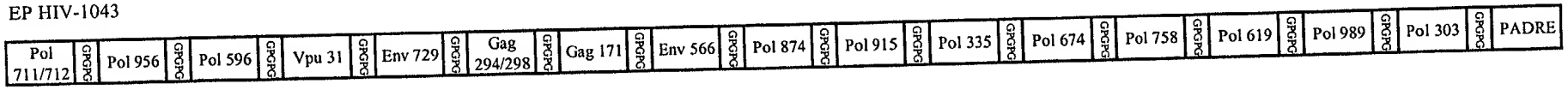
HIV 75mer



EP HIV-1043



EP HIV-1043



EP-HIV-1090

MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPKVSFEPIKIPIHYCAPA
KAKFVAAWTLKAAAKAFPVRPQVPLGAAKLTPLCVTLGAAAVLAEAMSQVKVYLAWVPAHKG
AAAAIFQSSMTKKTTLFCASDAKNIPYNPQSQGVVKHPVHAGPIANVTVYYGVPVWKKAAAQMA
VFIHNFKNAAAYPLASLRSLFNLTFGWCFKLNRILQQLLFINAKIQNFRVYYRKAAVTIKIGGQLKK
VPLQLPPLKAMTNNPPIPV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAAAGCTGGTGGGCAAACTCAACTGGGCCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGG
GGTGAATGCCGCTTGCCCTAAAGTCAGCTTCGAACCAATTAAGATCCCCATTCATTACTGTGC
ACCTGCCAAAGCTAAGTTTGTGGCCGCTTGGACCCTCAAGGCCGCTGCAAAAGCCTTCCCAGT
GAGGCCCCAGGTGCCTCTGGGCGCCGCTAAACTCACACCACTGTGCGTCACTCTGGGAGCCGC
TGCAGTGCTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGTGCCCGCCCACAA
GGGGGCCGCTGCAGCCATCTTTCAGTCTAGCATGACCAAGAAAACAACTCTGTTCTGTGCCTC
CGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGC
CGGACCTATTGCTAACGTGACCGTGTACTATGGGGTCCCAGTGTGGAAGAAAGCCGCTGCACA
GATGGCCGTGTTTATTCACAATTTCAAAAACGCCGCTGCATACCCCCTCGCCAGCCTGAGATC
CCTCTTCAACCTGACATTCGGCTGGTGCTTTAAGCTGAACCGGATCCTGCAGCAACTGCTCTTT
ATCAATGCTAAAATCCAGAACTTCCGCGTCTACTATAGGAAGGCTGCAGTGACTATCAAAATT
GGCGGACAACTGAAGAAAGTGCCTCTCCAGCTGCCCCCTCTCAAGGCAATGACCAACAATCC
CCCTATCCCAGTCTGA

HIV-CPT

MGMQVQIQSLFLLLLWVPGSRGIPIHYCAPAKAAKIQNFRVYYRKAAVTIKIGGQLKKAKFVAAW
TLKAAAKVPLQLPPLKAIFQSSMTKKLTPLCVTLGAQMAVFIHNFKGAKVYLAWVPAHKNAIPYN
PQSQGVVKAILKEPVHGVGAAALTFGWCFKLNAVLAEAMSQVNRILQQLLFINAAACPKVSFEPI
KVTVYYGVPVWKKAAHPVHAGPIANAAAYPLASLRSLFNAAATTLFCASDAKNKLVGKLNWAN
AAAFPVRPQVPLNMTNNPPIPV

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAATCCCCATTCACTACTGCGCCCCTGCTAAGGCAGCCAAAATCCAGAACTTCAGGGTGTAT
TACAGAAAGGCTGCAGTCACCATTAAAATCGGCGGACAACTGAAGAAAGCCAAGTTTGTGGC
CGCTTGGACACTCAAGGCCGCTGCAAAGGTCCCACTGCAGCTCCCCCCTCTGAAGGCCATCTT
CCAGAGCTCCATGACTAAGAAACTGACCCCACTGTGTGTGACACTCGGGGCCCAGATGGCTGT
GTTCATCCATAATTTTAAAGGCGCCAAGGTCTACCTGGCTTGGGTGCCCGCACACAAGAACGC
CATTCCTTACAATCCACAGTCTCAAGGAGTGGTCAAAGCTATTCTGAAGGAGCCCGTGCACGG
GGTGGGCGCCGCTGCACTCACTTTCGGATGGTGCTTTAAACTGAACGCCGTGCTGGCTGAAGC
CATGAGCCAGGTCAATCGGATCCTGCAGCAACTGCTCTTCATTAACGCCGCTGCATGTCCTAA
GGTGTCCTTCGAGCCAATCAAAGTGACCGTGTATTACGGGGTCCCCGTGTGGAAGAAAGCCGC
TCATCCTGTCCACGCAGGCCCAATCGCCAACGCCGCTGCATATCCCCTCGCCTCTCTGCGCAG
CCTGTTTAACGCCGCTGCAACAACCCTCTTTTGCGCCTCCGACGCTAAGAATAAACTGGTGGG
AAAGCTGAACTGGGCCAACGCAGCTGCATTCCCTGTGAGGCCACAGGTCCCCCTCAATATGAC
TAACAATCCCCCTATCCCAGTGTGA

09894168.1 DOCX

FIGURE 18A

HIV-FT

MQVQIQSLFLLLLWVPGSRGKLVGKLNWAMASDFNLPPVAIFQSSMTKVTIKIGGQLKRILQQLLF-
IMAVFIHNFKIPYNPQSQGVVTTLFCASDAKILKEPVHGVQMAVFIHNFKGAAVFIHNFKRCPKVSF
EPIKIQNFRVYYRLTFGWCFKLQVPLRPMTYKMTNNPPIPVTVYYGVPVWKVLAEAMSQVIPIHY
CAPAKLTPLCVTL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAAG
CTGGTGGGGAAGCTGAACTGGGCCATGGCCAGCGATTTCAACCTGCCCCCCGTGGCCATCTTC
CAGAGCAGCATGACCAAGGTGACCATCAAGATCGGGGGGCAGCTGAAGAGGATCCTGCAGCA
GCTGCTGTTCATCATGGCCGTGTTCATCCACAACTTCAAGATCCCCTACAACCCCCAGAGCCA
GGGGGTGGTGACCACCCTGTTCTGCGCCAGCGATGCCAAGATCCTGAAGGAGCCCGTGCACG
GGGTGCAGATGGCCGTGTTCATCCACAACTTCAAGGGCGCCGCCGTGTTCATCCACAACTTCA
AGAGGTGCCCCAAGGTGAGCTTCGAGCCCATCAAGATCCAGAACTTCAGGGTGTACTACAGG
CTGACCTTCGGGTGGTGCTTCAAGCTGCAGGTGCCCCTGAGGCCCATGACCTACAAGATGACC
AACAACCCCCCCATCCCCGTGACCGTGTACTACGGGGTGCCCGTGTGGAAGGTGCTGGCCGAG
GCCATGAGCCAGGTGATCCCCATCCACTACTGCGCCCCCGCCAAGCTGACCCCCCTGTGCGTG
ACCCTG

09604816 - 09604816

FIGURE 18B

HIV-TC

MGMQVQIQSLFLLLLWVPGSRGYWQATWIPEWKAIFQSSMTKKVYLAWVPAHKNAACPKVSFE
PIKHPVHAGPIANLTFGWCFKLNKMIGGIGGFIKFRDYVDRFYKAAARILQQLLFINTTLFCASDAK
NQMVHQAISPRGAKLVGKLNWAGAAAIYETYGDTWKAAQVPLRPMTYKGAAAVTVLDVGDAY
NAAARYLKDQQLLNTLNFPISPINMTNNPPIPVNAPYNTPVFAIKAAAVPLQLPPLKAAIPYNPQSQ
GVVKALLQLTVWGIGAAILKEPVHGVNAAAFPISPIETVKVWKEATTTLFKAAAVTIKIGGQLKKI
YQEPFKNLKAAAVLAEAMSQVNLVGPTPVNIGAAAEVNIVTDSQYKAAAIPIHYCAPAKAVIYQY
MDDLYKAAAQMAVFIHNFKNAATYQIYQEPFKPYNEWTLELKAKIQNFRVYYRKAFPVRPQVPL
GAAAIWGCSGKLIKVMIVWQVDRNAAKAACWWAGIKAKFVAAWTLKAAAKLTPLCVTLNAAM
ASDFNLPPVKSLLNATDIAVNVTVYYGVPVWKKAAAAIIRILQQLKRAMASDFNLNAAAYPLASL
RSLF

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCTAGA
GGATACTGGCAAGCTACTTGGATTCCAGAATGGAAAGCTATCTTTCAATCCTCAATGACGAAG
AAGGTATACCTGGCATGGGTCCCAGCACACAAGAACGCCGCTTGCCCAAAGGTGTCCTTTGAA
CCCATTAAACACCCAGTGCACGCAGGGCCAATAGCGAATTTGACATTCGGGTGGTGCTTCAAA
CTAAACAAAATGATCGGCGGCATTGGAGGCTTTATCAAGTTTAGAGATTACGTGGACCGATTC
TATAAAGCCGCTGCCCGTATACTCCAGCAGCTACTATTCATCAACACCACTCTCTTCTGCGCTT
CAGACGCTAAGAACCAAATGGTACACCAAGCCATAAGCCCTAGAGGAGCCAAGCTCGTAGGG
AAATTAAATTGGGCGGGTGCAGCAGCAATCTACGAGACTTACGGCGATACCTGGAAAGCAGC
CCAGGTTCCGTTACGCCCAATGACCTATAAAGGCGCAGCAGCAGTAACAGTTCTAGATGTAGG
AGACGCTTACAACGCTGCCGCAAGATACCTAAAAGATCAGCAGTTACTCAACACACTAAATTT
CCCAATTAGCCCGATAAACATGACAAATAACCCACCAATTCCCGTCAATGCTCCCTACAACAC
TCCAGTATTCGCAATCAAAGCCGCTGCTGTCCCCCTGCAGCTCCCTCCTCTGAAAGCTGCGAT
ACCTTACAACCCACAGAGCCAAGGTGTTGTCAAAGCACTGCTTCAGCTAACAGTTTGGGGAAT
TGGTGCTGCAATTCTAAAAGAGCCAGTTCATGGGGTTAACGCCGCCGCCTTCCCAATCAGTCC
TATTGAGACTGTGAAAGTATGGAAAGAAGCCACAACCACACTTTTTAAGGCAGCCGCAGTTA
CAATTAAAATAGGGGGCCAACTTAAGAAAATATACCAGGAACCTTTCAAGAATCTCAAAGCC
GCTGCAGTGCTCGCCGAGGCTATGTCACAGGTGAATTTGGTCGGACCAACACCCGTAAACATC
GGAGCCGCAGCCGAAGTGAACATAGTCACCGACTCACAGTACAAAGCCGCTGCAATACCCAT
ACATTATTGTGCTCCCGCAAAGGCCGTGATCTATCAATATATGGACGACCTGTATAAGGCCGC
CGCGCAGATGGCAGTCTTTATCCACAACTTTAAAAACGCAGCTACTTATCAGATCTACCAGGA
ACCATTCAAACCGTACAATGAGTGGACCTTGGAACTAAAGGCCAAAATTCAGAACTTCAGGG
TATATTATAGAAAAGCATTTCCAGTGAGGCCCCAGGTGCCTCTGGGTGCCGCAGCAATATGGG
GATGTTCTGGAAAACTGATCAAGGTGATGATTGTATGGCAAGTGGACAGAAATGCAGCTAAG
GCAGCCTGTTGGTGGGCAGGTATAAAAGCAAAGTTCGTGGCAGCATGGACGCTTAAAGCAGC
CGCAAAACTCACTCCTCTCTGCGTGACACTTAATGCAGCCATGGCCTCTGATTTCAACCTTCCC
CCTGTAAAATCCCTGCTTAATGCGACAGATATCGCAGTCAACGTAACAGTATATTATGGCGTG
CCAGTCTGGAAAAAAGCCGCCGCGGCCATAATTCGGATACTGCAGCAGCTGAAAAGAGCTAT
GGCGAGTGACTTCAACCTGAATGCGGCCGCCTACCCCTTGGCATCGTTAAGGTCACTATTTTG
A

Docket No. 95-0296.00

FIGURE 18C

HCV.1

MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVDLMGYIPLVYLVAYQATVILAGYGAGVRLIVFP
DLGVHMWNFISGIYLLPRRGPRLYLVTRHADVVLVGGVLAALLFLLLADAFLLLADARVWMNRL
IAFACTCGSSDLYLSAFSLHSYGVAGALVAFKLPGCSFSIFKTSERSQPRLIFCHSKKKFWAKHMW
NFIPFYGKAIRMYVGGVEHRQLFTFSPRRRLGVRATRKVGIYLLPNRAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGACTGC
TGTTCAACATCCTGGGGGGGTGGGTGGATCTGATGGGGTACATCCCCCTGGTGTACCTGGTGGCCTACCAGGCCACCGT
GATCCTGGCCGGGTACGGGGCCGGGGTGAGGCTGATCGTGTTCCCCGATCTGGGGGTGCACATGTGGAACTTCATCAGC
GGGATCTACCTGCTGCCCAGGAGAGGACCTAGACTGTACCTGGTGACTAGACACGCTGATGTGGTGCTGGTGGGAGGAG
TGCTGGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTTTCCTGCTGCTGGCTGATGCTAGAGTGTGGATGAACAGACT
GATCGCTTTCGCTTGTACATGTGGAAGCTCCGATCTGTATCTGAGCGCTTTCAGCCTGCACAGCTACGGAGTGGCTGGA
GCTCTGGTGGCTTTTAAGCTGCCTGGATGTAGCTTTAGCATCTTTAAGACCAGCGAAAGAAGCCAGCCTAGACTGATCT
TTTGTCACAGCAAGAAGAAGTTTTGGGCTAAGCACATGTGGAATTTTATCCCTTTCTATGGAAAGGCTATCAGAATGTA
TGTGGGAGGAGTGGAACACAGACAGCTGTTTACATTTAGCCCTAGAAGGAGACTGGGAGTGAGAGCTACAAGAAAGGTG
GGAATCTATCTGCTGCCTAATAGATGAAAGCTTGGG*

HCV.2

MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAALLFLLLADALIFCHSKKKQLF
TFSPRRYLVTRHADVYLLPRRGPRLCTCGSSDLYHMWNFISGIFWAKHMWNFAKFVAAWTLKAA
AILAGYGAGVYLVAYQATVGVAGALVAFKIPFYGKAIRMYVGGVEHRVLVGGVLAAFLLLADA
RVLPGCSFSIFAKFVAAWTLKAAAKTSERSQPRRLGVRATRKRLIVFPDLGVWMNRLIAFALSAFS
LHSYLLFNILGGWVVGIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGATCTGATGGGATATATCCCTCTGGTGGCTAAGTTTGTGGCTGCT
TGGACACTGAAGGCTGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTCTGATCTTCTGTCACA
GCAAGAAGAAGCAGCTGTTTACATTTAGCCCAAGAAGATATCTGGTGACAAGACACGCTGAT
GTGTATCTGCTGCCTAGACGCGGACCTAGACTGTGTACATGTGGAAGCTCCGATCTGTATCAC
ATGTGGAACTTTATCAGCGGAATCTTTTGGGCTAAGCACATGTGGAATTTCATCCTGGCTGGA
TATGGAGCTGGAGTGTATCTGGTGGCTTATCAGGCTACAGTGGGAGTGGCTGGAGCTCTGGTG
GCTTTCAAGATCCCATTCTATGGAAAGGCTATCAGAATGTATGTGGGAGGAGTGGAACACAG
AGTGCTGGTGGGAGGAGTGCTGGCTGCTTTCCTGCTGCTGGCTGATGCTAGAGTGCTGCCAGG
ATGTAGCTTTAGCATCTTCAAGACTTCCGAACGCTCCCAGCCTAGAAGACTGGGAGTGAGAGC
TACAAGGAAGAGACTGATCGTGTTTCCAGATCTGGGAGTGTGGATGAATAGACTGATCGCTTT
CGCTCTGAGCGCTTTCAGCCTGCACAGCTATCTGCTGTTCAACATCCTGGGAGGATGGGTGGT
GGGAATCTATCTGCTGCCAAACAGATGAAAGCTT

HCV.3s1

MGMQVQIQSLFLLLLWVPGSRGYLVAYQATVAKFVAAWTLKAAALLFLLLADALIFCHSKKKYL
VTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNF*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGATACCTCGTCGCCTACCAGGCCACTGTGGCTAAATTCGTGGCAGCC
TGGACACTGAAAGCTGCAGCTCTGCTCTTCCTGCTCCTGGCCGATGCACTCATCTTCTGCCATT
CCAAGAAAAAGTATCTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGC
AAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACTTTATTTCTGGAATCTTTTGGG
CCAAGCACATGTGGAATTTCTGAAAGCTT

FIGURE 18D

HCV.3s2
MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYIL
AGYGAGVWMNRLIAFAIPFYGKAIVAGALVAFKVGIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTCGCTGCT
TGGACACTGAAGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT
GCCATTCCATTCTATGGGAAAGCCATTGTGGCTGGCGCCCTGGTGGCATTCAAGGTCGGGATC
TACCTCCTGCCTAACCGCTGAAAGCTT

HCV.3s2(-3)
MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYIL
AGYGAGVWMNRLIAFA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTCGCTGCT
TGGACACTGAAGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT
GCCTGAGGATCC

HCV.3s3
MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAARLGVRATRKLLFNILGGWV
RMYVGGVEHRRLIVFPDLGVGVAGALVAFKLPGCSFSIFKTSERSQPRQLFTFSPRRYLLPRRGPRL

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGACCTGATGGGCTACATCCCTCTCGTGGCCAAGTTTGTGGCAGCT
TGGACCCTGAAGGCCGCTGCCAGACTGGGAGTGCGCGCTACACGGAAACTCCTGTTTAACATC
CTGGGAGGGTGGGTGCGGATGTACGTCGGAGGCGTCGAGCACAGAAGGCTCATTGTCTTTCC
AGATCTCGGCGTGGGCGTCGCAGGCGCACTCGTGGCCTTCAAACTGCCAGGGTGCAGCTTCAG
CATTTTCAAGACCTCCGAACGCTCCCAACCCAGACAGCTGTTCACTTTCTCTCCTCGGAGGTAT
CTGCTGCCCAGACGCGGACCCAGGCTGTGAAAGCTT

HCV.PC3
MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVKAKFVAAWTLKAAALADGGCSGGAYRLIVFPD
LGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCCAAGTTCGTG
GCTGCCTGGACCCTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCGGAGCTTACAG
GCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGAATTTCATCGG
GGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAAGACGGTGAGG
TACC

FIGURE 18E

HCV.PC4
MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAKFVAAWTLKAAAKTSERSQPRNLPGCSFSIFN
DLMGYIPLVKYLLPRRGPRLNTLCGFADLMGYRMYVGGVEHR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCCGGATCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCCAAGTTCGTGGC
TGCCTGGACCCTGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTG
GATGCTCTTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCC
CAGACGGGGCCCTCGCCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTA
TGTCGGCGGAGTCGAACACAGATGAGGTACC

HCV.2431(1P)
MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAFLLLADARVLSAFSLHSYILAGYGAGVWMNRL
IAFAGAAARLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVKYLLPRRGPRLNTLCG
FADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFPDLGVKFWAKHMWN
FIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLLADALIFCHSKKKYLVTRHADVLG
FGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKAAAAKFVAAWTLKAAA

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGCTCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCA
GACGCCAGGGTGCTGTCTGCCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGC
GTGTGGATGAATCGGCTGATCGCCTTTGCCGGCGCTGCCGCAAGGCTGGGCGTGAGAGCCACC
CGGAAGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTC
TTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGG
GGCCCTCGCCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGC
GGAGTCGAACACAGAAAACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCT
GGCCGACGGGGGATGCAGCGGCGGAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAA
ATTTTGGGCAAAGCACATGTGGAATTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAA
GCAGCTCTTCACCTTCTCCCCAAGACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGC
TGCAGCTCTGCTCTTCCTGCTCCTGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTAT
CTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGC
AGCTCCGACCTGTATCACATGTGGAACTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGG
AATTTTAAGGCCGCAGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGG
ATCC

Docket No. 2006-0168.02

FIGURE 18F

HCV.4312(1P)
MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVK-
YLLPRRGPRLNTLCGFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFP
DLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLLADALIFCHS
KKKYLVTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLAA
AFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFANAAAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGCTCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAAC
AAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCAT
GGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTCGCCTGAACACTCTCTG
TGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGCGGAGTCGAACACAGAAAACTGCT
CTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCG
GAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGA
ATTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAA
GACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGCTGCAGCTCTGCTCTTCCTGCTCC
TGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACG
TGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGT
GGAACTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGGAATTTTAAGAAAGCCGCTGCAG
TCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTG
CCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGA
TCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAG
GATCC

AOSI.K
MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVKFLLSLGIH
LYMDDVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWLSLLVPFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGAAGTTCCTGCTGTCCCTGGGAA
TCCACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT
TCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGTGA

HBV.1
MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVFLLSLGIHL
YMDDVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWLSLLVPFVIPIPSSWAFTP
ARVTGGVFKVGNFTGLYLPSDFFPSVTLWKAGILYKNVSIPWTHKLVVDFSQFSRSAICSVVRRAL
MPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGTTCCTGCTGTCCCTGGGAATCC
ACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCC
TGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGGCCT
TCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGATCCCTATCCCTAG
CTCCTGGGCTTTCACCCCAGCCAGGGTGACCGGAGGAGTGTTTAAGGTGGGAAACTTCACCGG
CCTGTATCTGCCCAGCGATTTCTTTCCTAGCGTGACCCTGTGGAAGGCCGGGATCCTGTACAA
GAATGTGTCCATCCCTTGGACCCACAAGCTGGTGGTGGACTTTTCCCAGTTCAGCAGATCCGC
TATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGTATGCCTGTATCTGA

FIGURE 18G

EL279505 US 20050096289A1

HBV.2
MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVNFLLSLGIH
LYMDDVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIP
SSWAFKTPARVTGGVFKVGNFTGLYNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDFSQ
FSRNSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGAACTTCCTGCTGTCCCTGGGAA
TCCACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT
TCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGT
GAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGAGTGTT
TAAGGTGGGAAACTTCACCGGCCTGTATAACCTGCCCAGCGATTTCTTTCCTAGCGTGAAGAC
CCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCG
CTCTGGTGGTGGACTTTTCCCAGTTCAGCAGAAATTCCGCTATCTGCTCCGTGGTGAGGAGAG
CTCTGATGCCACTGTATGCCTGTATCTGA

PfCTL.1
MQVQIQSLFLLLLWVPGSRGILSVSSFLFVNAAAQTNFKSLLRNLPSENERGYKAAALLACAGLAY
KKAAAAKFVAAWTLKAAAKAFMKAVCVEVNAAASFLFVEALFNATPYAGEPAPFKAAAKYKLA
TSVLKAGVSENIFLKNAAAYFILVNLLIKAGLLGVVSTV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAATCCTGAGCGTGTCCTCTTTCCTGTTTGTCAACGCCGCTGCACAGACCAATTTCAAGAGC
CTCCTGAGGAACCTCCCCTCCGAGAACGAAAGAGGCTACAAAGCCGCTGCACTGCTCGCCTGC
GCTGGACTGGCCTATAAGAAAGCCGCTGCAGCCAAGTTCGTGGCCGCTTGGACACTGAAGGC
CGCTGCAAAAGCCTTTATGAAGGCTGTCTGTGTGGAGGTCAATGCCGCTGCATCTTTCCTGTTT
GTGGAGGCCCTCTTTAACGCTACTCCTTACGCAGGGGAACCAGCCCCCTTCAAGGCCGCTGCA
AAATATAAGCTGGCAACCAGCGTGCTGAAGGCTGGCGTGTCCGAGAATATTTTTCTGAAAAAC
GCCGCTGCATACTTCATCCTGGTGAATCTGCTCATTAAGGCCGGACTCCTGGGGGTGGTCTCT
ACAGTGTGA

PfCTL.2
MQVQIQSLFLLLLWVPGSRGFVEALFQEYNAAAKYLVIVFLINALACAGLAYKKFYFILVNLLKA
ALFFIIFNKNAAAKFVAAWTLKAAAKFILVNLLIFHNFQDEENIGIYKLPYGRTNLKAAAVLLGGV
GLVLNFLIFFDLFLVKAVLAGLLGVV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGATTCGTGGAGGCCCTGTTTCAGGAATACAACGCCGCTGCAAAGTATCTCGTCATCGTGTTC
CTGATCAATGCTCTGGCATGCGCCGGCCTCGCTTACAAAAAGTTTTACTTCATTCTGGTCAACC
TGCTCAAGGCCGCTCTGTTCTTTATCATTTTCAATAAAAACGCCGCAGCTAAGTTTGTGGCCGC
ATGGACCCTGAAGGCCGCTGCAAAATTCATCCTCGTGAATCTGCTCATTTTTCACAACTTCCAA
GACGAGGAAAATATCGGAATTTATAAGCTGCCCTACGGGAGGACAAACCTGAAAGCCGCTGC
AGTCCTGCTCGGCGGAGTGGGGCTGGTGCTCAATTTTCTGATCTTCTTTGATCTGTTCCTGGTG
AAGGCCGTCCTGGCCGGCCTGCTCGGAGTCGTGTGA

FIGURE 18H

PfCTL.3
MQVQIQSLFLLLLWVPGSRGVFLIFFDLFLNAAAPSDGKCNLYKAAAVTCGNGIQVRKLFHIFDGD
NEIKAHVLSHNSYEKNYYGKQENWYSLKKILSVFFLANAAAKFIKSLFHIFKAAALYISFYFIKAKF
VAAWTLKAAAKAAAYYIPHQSSLKAAAGLIMVLSFL

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAGTGTTCCTGATCTTCTTTGACCTGTTCCTGAACGCCGCTGCACCCAGCGATGGCAAGTGC
AATCTCTACAAGGCCGCTGCAGTGACCTGTGGAAACGGGATTCAGGTCAGGAAACTCTTTCAC
ATCTTCGACGGCGATAACGAGATCAAGGCCCATGTGCTGTCCCACAATTCTTATGAAAAAAAC
TACTATGGAAAGCAAGAGAATTGGTACAGCCTGAAGAAAATTCTGTCCGTGTTCTTTCTCGCC
AACGCCGCTGCAAAGTTTATCAAGTCTCTGTTCCATATTTTCAAGGCCGCTGCACTCTACATCA
GCTTCTATTTTATTAAAGCCAAATTTGTGGCCGCTTGGACACTGAAGGCCGCTGCAAAAGCCG
CTGCATACTATATCCCTCACCAGAGCTCCCTGAAGGCCGCTGCAGGGCTGATCATGGTGCTCT
CTTTCCTGTGA

PfCTL/HTL(N)
MQVQIQSLFLLLLWVPGSRGSSVFNVVNSSIGLIMVLSFLGPGPGLYISFYFILVNLLIFHINGKIIKN
SEGPGPGPDSIQDSLKESRKLSGPGPGVLAGLLGVVSTVLLGGVGLVLGPGPGLPSENERGYYIPHQ
SSLGPGPGQTNFKSLLRNLGVSENIFLKGPGPGFQDEENIGIYGPGPGKYLVIVFLIFFDLFLVGPGP
GKFIKSLFHIFDGDNEIGPGPGKSKYKLATSVLAGLLGPGPGLPYGKTNLGPGPGRHNWVNHAVPL
AMKLIGPGPGMRKLAILSVSSFLFVEALFQEYGPGPGVTCGNGIQVRGPGPGMNYYGKQENWYSL
KKGPGPGPSDGKCNLYADSAWENVKNVIGPFMKAVCVEVGPGPGKILSVFFLALFFIIFNKGPGPG
HVLSHNSYEKGPGPGKYKIAGGIAGGLALLACAGLAYKFVVPGAATPYAGEPAPF

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAAGTAGTGTGTTCAATGTTGTGAACTCATCAATTGGTCTGATCATGGTGCTGAGCTTTCTCG
GGCCAGGGCCAGGATTATATATTTCTTTCTACTTCATCCTTGTCAACCTGTTAATATTCCACAT
TAACGGCAAAATAATAAAGAACAGTGAAGGCCCTGGGCCTGGGCCTGACTCGATCCAGGATT
CTCTAAAAGAATCGAGGAAGCTCTCCGGACCAGGCCCTGGTGTACTCGCCGGGTTGCTGGGA
GTAGTTAGCACAGTGCTGTTAGGAGGCGTCGGCCTCGTCTTAGGACCTGGACCAGGTCTGCCG
TCCGAAAACGAAAGAGGATACTACATACCTCACCAGAGCAGCCTCGGCCCAGGCCCCGGACA
AACCAATTTCAAATCCCTCTTGCGAAATCTAGGAGTGAGCGAGAACATATTTCTTAAAGGACC
CGGTCCCGGCTTTCAGGACGAGGAGAATATAGGTATTTACGGTCCAGGACCTGGAAAATACCT
AGTGATCGTATTCCTAATTTTTTTTGACCTATTTCTGGTGGGCCCAGGTCCCGGAAAGTTCATT
AAATCACTCTTCCACATTTTTGACGGAGATAACGAGATAGGACCCGGTCCCGGGAAATCAAA
GTACAAACTAGCCACTTCAGTGCTGGCCGGCCTTCTAGGGCCGGGCCCAGGGCTCCCCTATGG
AAAGACAAATCTTGGCCCCGGTCCAGGACGGCACAACTGGGTGAATCATGCGGTTCCATTGG
CCATGAAACTAATCGGGCCCGGTCCAGGCATGCGCAAACTTGCAATTCTAAGCGTAAGTTCAT
TTCTGTTCGTAGAGGCACTGTTTCAAGAATATGGCCCAGGACCTGGCGTCACATGTGGGAATG
GGATCCAGGTGAGAGGACCGGGACCTGGTATGAACTATTACGGTAAACAGGAAAATTGGTAC
TCCCTGAAAAAGGGTCCAGGCCCCGGCCCCTCAGATGGTAAGTGCAACCTGTATGCTGACTCA
GCATGGGAGAACGTAAAAAATGTAATAGGCCCATTCATGAAGGCAGTTTGTGTCGAAGTCGG
ACCAGGCCCAGGAAAAATACTTTCTGTCTTCTTCCTAGCTCTCTTCTTCATCATCTTCAACAAG
GGACCAGGGCCAGGTCACGTGTTATCCCATAACTCTTATGAAAAAGGGCCAGGACCTGGGAA
ATACAAAATCGCAGGAGGGATCGCCGGCGGGCTAGCGCTCCTTGCCTGCGCAGGCTTGGCTTA
CAAATTCGTTGTACCAGGAGCTGCAACACCCTATGCAGGAGAACCTGCCCCATTTTGAAGATC
TGC

Docket No. 0505.0021-00

FIGURE 18I

Pf33

MGMQVQIQSLFLLLLWVPGSRGFMKAVCVEVNVTCGNGIQVRKGLIMVLSFLNAALFHIFDGDN
EIKAALLACAGLAYKKSFLFVEALFNAAPSDGKCNLYKAAQTNFKSLLRNLPSENERGYKAAGVS
ENIFLKNAAAYFILVNLLIKAAAILSVSSFLFVNTPYAGEPAPFKAAAKYKLATSVLKAAVFLIFFDL
FLNYYIPHQSSLKAAGLLGNVSTVGAVLLGGVGLVLNLACAGLAYKKAKFIKSLFHIFKAAFYFIL
VNLLKAFLIFFDLFLVKALFFIIFNKNYYGKQENWYSLKFVEALFQEYNAAAKFVAAWTLKAAAK
ILSVFFLANAVLAGLLGNVNFQDEENIGIYKAAALYISFYFIKAFILVNLLIFHNAALPYGRTNLKAA
HVLSHNSYEKNAAAKYLVIVFLI

GCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCC
GGATCCAGAGGATTTATGAAAGCTGTCTGTGTAGAGGTGAATGTAACATGCGGTAACGGAAT
TCAGGTGAGAAAGGGACTCATCATGGTACTCAGCTTTCTGAACGCAGCCCTGTTCCACATCTT
TGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCCGGACTAGCCTATAAAAAGA
GTTTCCTTTTCGTTGAAGCACTATTTAACGCAGCACCCAGTGACGGTAAATGCAACCTATATA
AAGCAGCTCAGACTAATTTCAAAAGCCTGTTAAGAAATCTGCCCTCAGAGAATGAAAGGGGT
TACAAAGCCGCCGGCGTGTCCGAGAATATTTTCCTGAAGAACGCCGCTGCTTATTTTATACTC
GTGAATCTACTCATAAAGGCAGCCGCAATCCTTTCAGTGTCCAGCTTTCTGTTTGTTAACACAC
CATATGCGGGCGAGCCGGCTCCTTTCAAGGCTGCAGCAAAATACAAGCTTGCCACATCAGTAT
TGAAAGCAGCTGTGTTTTTGATATTCTTTGATCTTTTTTTAAACTACTACATACCTCATCAGTCT
AGTCTTAAAGCAGCCGGGCTACTGGGGAACGTCTCTACTGTGGGGGCCGTCTTACTTGGAGGA
GTTGGCCTCGTGTTGAACCTCGCGTGCGCAGGTCTGGCCTACAAAAAAGCGAAATTCATCAAG
TCTCTGTTCCACATTTTTAAAGCCGCATTCTATTTCATACTAGTGAACCTTCTCAAAGCTTTCCT
GATCTTCTTCGATCTATTCCTCGTAAAAGCGCTATTCTTCATTATCTTTAACAAAAATTATTAC
GGCAAGCAAGAAAATTGGTACTCACTCAAGTTTGTAGAAGCTCTGTTCCAGGAATACAACGCC
GCTGCTAAATTCGTTGCAGCTTGGACCCTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTTC
TCGCTAATGCCGTATTAGCAGGACTTCTAGGCAACGTGAACTTTCAAGACGAAGAGAATATAG
GCATCTACAAAGCCGCAGCACTGTACATTTCATTCTACTTCATCAAGGCCTTCATACTGGTCAA
CCTTCTGATATTTCATAATGCAGCACTGCCATATGGGAGAACCAACTTGAAAGCGGCCCACGT
GTTGAGCCACAACTCCTACGAGAAGAACGCCGCCGCGAAATATCTCGTCATTGTCTTCCTGAT
TTGA

TB.1

MQVQIQSLFLLLLWVPGSRGRMSRVTTFTVKALVLLMLPVVNLMIGTAAAVVKALVLLMLPVGA
GLMTAVYLVGAAAMALLRLPVKRMFAANLGVNSLYFGGICVGRLPLVLPAVNAAAAKFVAAWT
LKAAAKAAARLMIGTAAAGFVVALIPLVNAMTYAAPLFVGAAAAMALLRLPLV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAGG
ATGAGCAGAGTGACCACATTCACTGTCAAGGCCCTGGTGCTCCTGATGCTCCCCGTCGTGAAC
CTGATGATCGGCACCGCTGCAGCCGTCGTGAAAGCTCTCGTCCTGCTCATGCTCCCTGTGGGA
GCAGGGCTGATGACAGCCGTGTACCTGGTCGGCGCTGCAGCCATGGCCCTCCTGCGGCTGCCA
GTGAAGCGCATGTTTGCTGCAAATCTGGGAGTCAACTCCCTCTATTTCGGGGGCATTTGCGTG
GGAAGGCTGCCCCTCGTGCTGCCTGCTGTGAATGCAGCCGCTGCCAAATTTGTCGCCGCTTGG
ACTCTGAAGGCAGCCGCTAAGGCCGCTGCAAGACTGATGATCGGGACCGCCGCTGCCGGCTT
CGTGGTCGCCCTGATTCCCCTGGTGAACGCCATGACATACGCAGCTCCTCTGTTTGTGGGAGC
CGCTGCAGCCATGGCTCTCCTGCGGCTGCCACTGGTGTGA

FIGURE 18J

BCL A2 #90
MQVQIQSLFLLLLWVPGSRGIMIGHLVGVNRLLQETELVNAKVAEIVHFLNAKVFGSLAFVNAYL-
SGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGTRVNAAA
ATVGIMIGVNAKLCPVQLWV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAATT
ATGATCGGCCATCTGGTGGGCGTCAACAGACTGCTGCAGGAAACCGAGCTGGTGAATGCCAA
GGTGGCCGAAATTGTGCACTTTCTCAACGCAAAGGTGTTTGGTTCCCTGGCTTTTGTCAATGCC
TATCTGAGCGGCGCTAACCTCAACGTCGGAGCCGCCTACCTCCAGCTGGTCTTCGGCATCGAG
GTCAACGCTGCTGCAAAATTCGTGGCAGCTTGGACCCTCAAGGCTGCAGCAAAGGCTGCCGCC
GTCGTGCTCGGAGTGGTGTTCGGGATCAACTCTATGCCACCTCCCGGGACTAGGGTCAATGCT
GCCGCCGCAACAGTGGGAATCATGATTGGGGTGAATGCCAAACTGTGCCCAGTGCAACTGTG
GGTGTGA

BCL A2 #88
MQVQIQSLFLLLLWVPGSRGVVLGVVFGINAAAAKFVAAWTLKAAAKVAEIVHFLNAYLSGANL
NVGAAYLQLVFGIEVNIMIGHLVGVNRLLQETELVNAKVFGSLAFVNAKLCPVQLWVNAAAATV
GIMIGVNSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAGTC
GTGCTGGGAGTCGTCTTCGGCATTAATGCCGCCGCTGCAAAGTTCGTGGCTGCCTGGACCCTG
AAGGCCGCAGCTAAAGTGGCAGAGATCGTGCACTTTCTGAACGCCTACCTGAGCGGAGCAAA
TCTGAACGTCGGCGCTGCCTATCTGCAGCTCGTGTTTGGAATTGAAGTGAACATCATGATTGG
ACATCTGGTGGGCGTGAACAGGCTGCTCCAGGAAACTGAGCTGGTCAACGCTAAAGTGTTCG
GGTCTCTCGCCTTTGTGAACGCTAAGCTCTGCCCCGTCCAACTCTGGGTCAATGCCGCAGCCG
CTACAGTGGGGATCATGATCGGCGTGAACTCCATGCCTCCACCAGGGACCAGAGTGTGA

BCL A2 #63
MQVQIQSLFLLLLWVPGSRGKLCPVQLWVNAAAATVGIMIGVNIMIGHLVGVNRLLQETELVNA
KVAEIVHFLNAKVFGSLAFVNAYLSGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAA
AVVLGVVFGINSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAAAG
CTCTGCCCCGTGCAACTGTGGGTCAACGCCGCCGCCGCAACCGTCGGCATTATGATCGGGGTG
AACATCATGATCGGACACCTGGTCGGCGTGAACAGGCTGCTGCAGGAGACAGAACTGGTCAA
TGCCAAGGTGGCTGAAATTGTCCATTTCCTGAATGCCAAAGTGTTCGGCTCTCTCGCTTTCGTG
AACGCTTATCTGAGCGGAGCTAACCTCAACGTGGGGGCCGCATACCTCCAGCTCGTCTTTGGG
ATTGAGGTGAATGCCGCAGCTAAATTTGTCGCTGCCTGGACCCTGAAGGCAGCAGCCAAGGCT
GCCGCAGTGGTGCTGGGAGTGGTGTTTGGAATCAATTCCATGCCTCCACCAGGCACTAGAGTG
TGAGGATCC

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FIGURE 18K

Prostate 1
LTFFWLDRSVKAAAVLVHPQWVLTVKAAALLQERGVAYIKAALLLSIALSVNPLVCNGVLQGVK
AAIMYSAHDTTVKAAAFLTPKKLQCVNAMMNDQLMFLNAGLPSIPVHPVKAAALGTTCYVGAAI
LLWQPIPVNFLRPRSLQCVKAFLTLSVTWIGVNALLYSLVHNLGAATLMSAMTNL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATTG
ACATTTTTTTGGCTGGATAGATCGGTTAAGGCTGCAGCCGTGCTTGTTCATCCCCAGTGGGTCT
TGACCGTAAAGGCTGCCGCGCTGCTACAAGAAAGAGGGGTCGCATACATCAAAGCTGCTCTC
CTCTTGAGTATTGCGCTAAGTGTAAACCCGCTAGTTTGTAATGGGGTGTTACAAGGTGTGAAA
GCGGCGATTATGTACAGTGCCCACGACACTACCGTAAAAGCAGCCGCTTTCCTGACCCCAAAA
AAACTCCAATGCGTGAACGCAATGATGAATGATCAGCTGATGTTTTTAAACGCTGGCTTACCT
TCTATACCGGTTCATCCAGTCAAGGCCGCGGCATTGGGTACGACGTGTTATGTTGGAGCAGCG
ATACTTCTTTGGCAGCCCATACCAGTAAATTTTTTAAGACCTAGATCCTTACAATGCGTCAAAG
CATTCCTTACACTCTCAGTAACTTGGATCGGAGTCAATGCTCTGCTATATAGCCTCGTACACAA
CTTGGGCGCGGCCACACTTATGAGTGCAATGACGAATTTAGCTAAGTTCGTGGCGGCCTGGAC
TCTAAAGGCCGCAGCA

HIV-1043
MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGPGPGWEFVNTPPLVKLWYQGPGPGYR
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGPGPGGEIYKRWIILGLNKIVRMYGPGPGQGQM
VHQAISPRTLNGPGPGIKQFINMWQEVGKAMYGPGPGWAGIKQEFGIPYNPQGPGPGKTAVQMA
VFIHNFKRGPGPGSPAIFQSSMTKILEPGPGPGEVNIVTDSQYALGIIGPGPGHSNWRAMASDFNLPP
GPGPGAETFYVDGAANRETKGPGPGGAVVIQDNSDIKVVPGPGPGFRKYTAFTIPSINNE

ATGGAGAAGGTGTACCTGGCCTGGGTTCCAGCCCACAAAGGCATCGGGGGAGGGCCCGGACC
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG
GTTGGGAGTTTGTGAACACACCACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGAT
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCGGGCCCAGGCCAG
CACCTTCTGCAGCTTACAGTGTGGGGAATTAAACAGCTGCAGGGGCCGGGCCCCGGGGGGGA
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGCCCAG
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG
GATGGGCAGGGATAAAACAGGAGTTTGGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGT
AAAACGGCAGTGCAGATGGCCGTGTTCATTCATAATTTTAAGCGGGGCCCTGGACCTGGCAGC
CCAGCTATATTTCAAAGTTCGATGACCAAAATCTTGGAGCCCGGCCCAGGGCCGGGCGAAGT
GAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCAGGGCATTCCAA
TTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAAACTTT
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCA
TTCAGGACAACTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCCGGGTTCAGAAAGTATACCG
CCTTCACTATTCCGTCCATCAACAATGAGTGA

FIGURE 18L

HIV-1043 PADRE

MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGPGPGWEFVNTPPLVKLWYQGPGPGYR
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGPGPGGEIYKRWIILGLNKIVRMYGPGPGQGQM
VHQAISPRTLNGPGPGIKQFINMWQEVGKAMYGPGPGWAGIKQEFGIPYNPQGPGPGKTAVQMA
VFIHNFKRGPGPGSPAIFQSSMTKILEPGPGPGEVNIVTDSQYALGIIGPGPGHSNWRAMASDFNLPP
GPGPGAETFYVDGAANRETKGPGPGGAVVIQDNSDIKVVPGPGPGFRKYTAFTIPSINNEGPGPGA
KFVAAWTLKAAA

ATGGAGAAGGTGTACCTGGCCTGGGTTCCAGCCCACAAAGGCATCGGGGGAGGGCCCGGACC
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG
GTTGGGAGTTTGTGAACACACCACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGAT
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCGGGCCCAGGCCAG
CACCTTCTGCAGCTTACAGTGTGGGGAATTAAACAGCTGCAGGGGCCGGGCCCCGGGGGGGA
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGCCCAG
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG
GATGGGCAGGGATAAAACAGGAGTTTGGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGT
AAAACGGCAGTGCAGATGGCCGTGTTCATTCATAATTTTAAGCGGGGCCCTGGACCTGGCAGC
CCAGCTATATTTCAAAGTTCGATGACCAAAATCTTGGAGCCCGGCCCAGGGCCGGGCGAAGT
GAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCAGGGCATTCCAA
TTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAAACTTT
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCA
TTCAGGACAACTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCCGGGTTCAGAAAGTATACCG
CCTTCACTATTCCGTCCATCAACAATGAGGGCCCCGGCCCAGGTGCCAAGTTCGTGGCTGCCT
GGACCCTGAAGGCTGCCGCTTGA

HIV 75mer

EKVYLAWVPAHKGIGGPGPGQGQMVHQAISPRTLNGPGPGSPAIFQSSMTKILEPGPGPGFRKYTA
FTIPSINNE

GAGAAGGTGTACCTGGCCTGGGTGCCTGCCCACAAGGGAATCGGAGGACCTGGCCCTGGACA
GGGACAGATGGTGCACCAGGCCATCAGCCCTAGGACCCTGAACGGACCTGGACCTGGAAGCC
CTGCCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCGGACCTGGACCTGGATTCAGGA
AGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGTGA

FIGURE 18M

PfHTL

MQVQIQSLFLLLLWVPGSRGRHNWVNHAVPLAMKLIGPGPGKCNLYADSAWENVKNGPGPGKS-
KYKLATSVLAGLLGPGPGQTNFKSLLRNLGVSEGPGPGSSVFNVVNSSIGLIMGPGPGVKNVIGPF
MKAVCVEGPGPGMNYYGKQENWYSLKKGPGPGGLAYKFVVPGAATPYGPGPGPDSIQDSLKESR
KLNGPGPGLLIFHINGKIIKNSEGPGPGAGLLGNVSTVLLGGVGPGPGKYKIAGGIAGGLALLGPGP
GMRKLAILSVSSFLFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAAGGCACAACTGGGTGAATCATGCTGTGCCCCTGGCTATGAAGCTGATCGGCCCTGGACC
AGGGAAATGCAACCTCTACGCAGACAGCGCCTGGGAGAACGTCAAGAATGGCCCCGGACCTG
GGAAATCCAAGTATAAGCTCGCTACCTCTGTGCTGGCAGGCCTGCTCGGACCAGGCCCCGGAC
AGACAAATTTCAAAAGCCTGCTCAGAAACCTGGGAGTGTCCGAGGGGCCTGGCCCAGGATCT
AGCGTCTTTAATGTGGTCAACTCCTCTATTGGGCTCATCATGGGACCCGGACCTGGGGTGAAA
AATGTCATTGGCCCATTCATGAAGGCCGTGTGTGTCGAAGGACCCGGGCCTGGCATGAACTAC
TATGGAAAGCAAGAAAATTGGTACAGCCTGAAGAAAGGCCCTGGGCCAGGCGGACTGGCTTA
CAAGTTTGTGGTCCCAGGGGCAGCCACTCCCTATGGGCCTGGGCCAGGCCCCGATTCCATCCA
GGACTCTCTCAAAGAGAGCCGGAAACTGAACGGACCCGGGCCTGGACTGCTCATTTTCCACAT
CAATGGCAAAATTATCAAGAACAGCGAGGGACCTGGGCCAGGCGCCGGACTGCTGGGGAACG
TGTCCACCGTCCTGCTCGGCGGAGTGGGGCCCGGCCCTGGGAAGTACAAGATCGCTGGAGGG
ATCGCAGGCGGACTGGCCCTCCTGGGCCCAGGACCAGGGATGCGCAAACTGGCTATTCTCTCT
GTCTCCAGCTTTCTGTTTGTGTGA

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FIGURE 18N

Protein	Sequence	Restriction
HIV gag 386	VLAEAMSQV	HLA-A2
HIV gag 271	MTNNPPIPV	HLA-A2
HIV pol 774	MASDFNLPPV	HLA-A2
HIV pol 448	KLVGKLNWA	HLA-A2
HIV pol 163	LVGPTPVNI	HLA-A2
HIV pol 498	ILKEPVHGV	HLA-A2
HIV pol 879	KAACWWAGI	HLA-A2
HIV pol 132	KMIGGIGGFI	HLA-A2
HIV pol 772	RAMASDFNL	HLA-A2
HIV pol 183	TLNFPISPI	HLA-A2
HIV env 134	KLTPLCVTL	HLA-A2
HIV env 651	LLQLTVWGI	HLA-A2
HIV env 163	SLLNATDIAV	HLA-A2
HIV nef 221	LTFGWCFKL	HLA-A2
HIV vpr 59	AIIRILQQL	HLA-A2
HIV vpr 62	RILQQLLFI	HLA-A2
HIV pol 929	QMAVFIHNFK	HLA-A3
HIV pol 722	KVYLAWVPAHK	HLA-A3
HIV pol 971	KIQNFRVYYR	HLA-A3
HIV pol 347	AIFQSSMTK	HLA-A3
HIV pol 98	VTIKIGGQLK	HLA-A3
HIV env 61	TTLFCASDAK	HLA-A3
HIV env 47	VTVYYGVPVWK	HLA-A3
HIV nef 100	QVPLRPMTYK	HLA-A3
HIV vif 7	VMIVWQVDR	HLA-A3
HIV gag 162	QMVHQAISPR	HLA-A3
HIV gag 545	YPLASLRSLF	HLA-B7
HIV gag 237	HPVHAGPIA	HLA-B7
HIV pol 186	FPISPIETV	HLA-B7
HIV pol 893	IPYNPQSQGVV	HLA-B7
HIV env 259	IPIHYCAPA	HLA-B7
HIV env 250	CPKVSFEPI	HLA-B7
HIV nef 94	FPVRPQVPL	HLA-B7
HIV rev 75	VPLQLPPL	HLA-B7
HIV pol 684	EVNIVTDSQY	HLA-A1
HIV gag 317	FRDYVDRFY	HLA-A1
HIV pol 368	VIYQYMDDLY	HLA-A1
HIV pol 295	VTVLDVGDAY	HLA-A1
HIV pol 533	IYQEPFKNL	HLA-A24
HIV pol 244	PYNTPVFAI	HLA-A24
HIV pol 530	TYQIYQEPF	HLA-A24
HIV pol 597	YWQATWIPEW	HLA-A24
HIV env 681	IWGCSGKLI	HLA-A24
HIV env 671	RYLKDQQLL	HLA-A24

FIGURE 19A

Protein	Sequence	Restriction
HIV env 55	VWKEATTTLF	HLA-A24
HIV vpr 46	IYETYGDTW	HLA-A24
HIV vpr 14	PYNEWTLEL	HLA-A24
HIV gag 298	KRWIILGLNKIVRMY	HLA-DR
HIV pol 596	WEFVNTPPLVKLWYQ	HLA-DR
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR
HIV pol 712	KVYLAWVPAHKGIGG	HLA-DR
HIV gag 294	GEIYKRWIILGLNKI	HLA-DR
HIV pol 711	EKVYLAWVPAHKGIG	HLA-DR
HIV env 729	QHLLQLTVWGIKQLQ	HLA-DR
HIV gag 171	QGQMVHQAISPRTLN	HLA-DR
HIV pol 335	SPAIFQSSMTKILEP	HLA-DR
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR
HIV pol 303	FRKYTAFTIPSINNE	HLA-DR
HIV pol 758	HSNWRAMASDFNLPP	HLA-DR
HIV pol 915	KTAVQMAVFIHNFKR	HLA-DR
HIV vpu 31	YRKILRQRKIDRLID	HLA-DR3
HIV pol 874	WAGIKQEFGIPYNPQ	HLA-DR3
HIV pol 674	EVNIVTDSQYALGII	HLA-DR3
HIV pol 619	AETFYVDGAANRETK	HLA-DR3
HIV pol 989	GAVVIQDNSDIKVVP	HLA-DR3
HCV NS4 1812	LLFNILGGWV	HLA-A2
HCV NS1/E2 728	FLLLADARV	HLA-A2
HCV NS4 1590	YLVAYQATV	HLA-A2
HCV NS5 2611	RLIVFPDLGV	HLA-A2
HCV CORE 132	DLMGYIPLV	HLA-A2
HCV NS4 1920	WMNRLIAFA	HLA-A2
HCV NS4 1666	VLVGGVLAA	HLA-A2
HCV NS4 1769	HMWNFISGI	HLA-A2
HCV NS4 1851	ILAGYGAGV	HLA-A2
HCV CORE 35	YLLPRRGPRL	HLA-A2
HCV NS1/E2 726	LLFLLLADA	HLA-A2
HCV LORF 1131	YLVTRHADV	HLA-A2
HCV CORE 51	KTSERSQPR	HLA-A3
HCV CORE 43	RLGVRATRK	HLA-A3
HCV ENV1 290	QLFTFSPRR	HLA-A3
HCV NS1/E2 632	RMYVGGVEHR	HLA-A3
HCV NS3 1396	LIFCHSKKK	HLA-A3
HCV NS4 1863	GVAGALVAFK	HLA-A3
HCV NS4 1864	VAGALVAFK	HLA-A3
HCV NS3 1262	LGFGAYMSK	HLA-A3
HCV Core 169	LPGCSFSIF	HLA-B7
HCV NS5 2922	LSAFSLHSY	HLA-A1
HCV NS3 1128	CTCGSSDLY	HLA-A1
HCV NS5 2180	LTDPSHITA	HLA-A1

FIGURE 19B

Protein	Sequence	Restriction
HCV Core 126	LTCGFADLMGY	HLA-A1
HCV NS3 1305	LADGGCSGGAY	HLA-A1
HCV NS4 1765	FWAKHMWNF	HLA-A24
HCV NS5 2875	RMILMTHFF	HLA-A24
HCV NS5 2639	VMGSSYGF	HLA-A24
HCV NS4 1765	FWAKHMWNFI	HLA-A24
P. falciparum SSP2-230	FMKAVCVEV	HLA-A2
P. falciparum EXP1-83	GLLGVVSTV	HLA-A2
P. falciparum CSP-7	ILSVSSFLFV	HLA-A2
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3
P. falciparum LSA1-105	GVSENIFLK	HLA-A3
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7
P. falciparum LSA1-1663	LPSENERGY	HLA-A1
P. falciparum EXP1-73	KYKLATSVL	HLA-A24
P. falciparum CSP-12	SFLFVEALF	HLA-A24
P. falciparum LSA1-10	YFILVNLLI	HLA-A24
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2
P. falciparum SSP2-523	LACAGLAYK	HLA-A3
P. falciparum EXP1-10	ALFFIIFNK	HLA-A3
P. falciparum LSA1-11	FILVNLLIFH	HLA-A3
P. falciparum SSP2-126	LPYGRTNL	HLA-B7
P. falciparum CSP-15	FVEALFQEY	HLA-A1
P. falciparum LSA1-1794	FQDEENIGIY	HLA-A1
P. falciparum LSA1-9	FYFILVNLL	HLA-A24
P. falciparum SSP2-8	KYLVIVFLI	HLA-A24
P. falciparum CSP-394	GLIMVLSFL	HLA-A2
P. falciparum EXP1-2	KILSVFFLA	HLA-A2
P. falciparum CSP-344	VTCGNGIQVR	HLA-A3
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1
P. falciparum LSA1-1671	YYIPHQSSL	HLA-A24
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24
P. falciparum LSA1-1881	LFHIFDGDNEI	HLA-A24
P. falciparum CSP-55	YYGKQENWYSL	HLA-A24
P. falciparum LSA1-5	LYISFYFI	HLA-A24
P. falciparum CSP-2	MRKLAILSVSSFLFV	HLA-DR
P. falciparum CSP-53	MNYYGKQENWYSLKK	HLA-DR
P. falciparum CSP-375	SSVFNVVNSSIGLIM	HLA-DR
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3

FIGURE 19C

Protein	Sequence	Restriction
P. falciparum SSP2-223	VKNVIGPFMKAVCVE	HLA-DR
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR
P. falciparum SSP2-527	GLAYKFVVPGAATPY	HLA-DR
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR
P. falciparum LSA1-16	LLIFHINGKIIKNSE	HLA-DR
P. falciparum LSA1-94	QTNFKSLLRNLGVSE	HLA-DR
HBV core 18	FLPSDFFPSV	HLA-A2
HBV env 183	FLLTRILTI	HLA-A2
HBV env 335	WLSLLVPFV	HLA-A2
HBV pol 455	GLSRYVARL	HLA-A2
HBV pol 538	YMDDVVLGV	HLA-A2/A1
HBV pol 773	ILRGTSFVYV	HLA-A2
HBV pol 562	FLLSLGIHL	HLA-A2
HBV pol 642	ALMPLYACI	HLA-A2
HBV env 338	GLSPTVWLSV	HLA-A2
HBV core 141	STLPETTVVRR	HLA-A3
HBV pol 149	HTLWKAGILYK	HLA-A3/A1
HBV pol 150	TLWKAGILYK	HLA-A3
HBV pol 388	LVVDFSQFSR	HLA-A3
HBV pol 47	NVSIPWTHK	HLA-A3
HBV pol 531	SAICSVVRR	HLA-A3
HBV pol 629	KVGNFTGLY	HLA-A3/A1
HBV pol 665	QAFTFSPTYK	HLA-A3
HBV core 19	LPSDFFPSV	HLA-B7
HBV env 313	IPIPSSWAF	HLA-B7
HBV pol 354	TPARVTGGVF	HLA-B7
TB	RMSRVTTFTV	HLA-A2
TB	ALVLLMLPVV	HLA-A2
TB	LMIGTAAAVV	HLA-A2
TB	ALVLLMLPV	HLA-A2
TB	GLMTAVYLV	HLA-A2
TB	MALLRLPV	HLA-A2
TB	RMFAANLGV	HLA-A2
TB	SLYFGGICV	HLA-A2
TB	RLPLVLPAV	HLA-A2
TB	RLMIGTAAA	HLA-A2
TB	FVVALIPLV	HLA-A2
TB	MTYAAPLFV	HLA-A2
TB	AMALLRLPLV	HLA-A2
p53 139	KLCPVQLWV	HLA-A2
CEA 687	ATVGIMIGV	HLA-A2
CEA 691	IMIGHLVGV	HLA-A2
Her2/neu 689	RLLQETELV	HLA-A2
MAGE3 112	KVAEIVHFL	HLA-A2

FIGURE 19D

Protein	Sequence	Restriction
Her2/neu 369	KVFGSLAFV	HLA-A2
CEA 605	YLSGANLNV	HLA-A2
MAGE2 157	YLQLVFGIEV	HLA-A2
Her2/neu 665	VVLGVVFGI	HLA-A2
p53 149	SMPPPGTRV	HLA-A2
PAP.21.T2	LTFFWLDRSV	HLA-A2
PAP.112	TLMSAMTNL	HLA-A2
PAP.284	IMYSAHDTTV	HLA-A2
PSM.288.V10	GLPSIPVHPV	HLA-A2
PSM.441	LLQERGVAYI	HLA-A2
PSM.469L2	LLYSLVHNL	HLA-A2
PSM.663	MMNDQLMFL	HLA-A2
PSA.3.V11	FLTLSVTWIGV	HLA-A2
PSA.143.V8	ALGTTCYV	HLA-A2
PSA.161	FLTPKKLQCV	HLA-A2
HuK2.4.L2	LLLSIALSV	HLA-A2
HuK2.53.V11	VLVHPQWVLTV	HLA-A2
HuK2.165	FLRPRSLQCV	HLA-A2
HuK2.216.V11	PLVCNGVLQGV	HLA-A2

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FIGURE 19E